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(54) Title: METHODS AND REAGENTS FOR DISCOVERING AND USING MAMMALIAN MELANOCORTIN RECEPTOR AGONISTS AND ANTAGONISTS TO MODULATE FEEDING BEHAVIOR IN ANIMALS		
(57) Abstract <p>The present invention provides recombinant expression constructs comprising nucleic acid encoding mammalian melanocortin receptors, and mammalian cells into which said recombinant expression constructs have been introduced that express functional mammalian melanocortin receptors. The invention provides a panel of such transformed mammalian cells expressing melanocortin receptors for screening compounds for receptor agonist and antagonist activity. The invention also provides methods for using such panels of melanocortin receptor-expressing mammalian cells to specifically detect and identify agonists and antagonists for each melanocortin receptor, as well as patterns of agonist and antagonist activity of said compounds for the class of melanocortin receptors. Such screening methods provide a means for identifying compounds with patterns of melanocortin agonist and antagonist activity which is associated with the capacity to influence or modify metabolism and behavior, particularly feeding behavior.</p>		

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**METHODS AND REAGENTS FOR DISCOVERING AND USING
MAMMALIAN MELANOCORTIN RECEPTOR AGONISTS AND
ANTAGONISTS TO MODULATE FEEDING BEHAVIOR IN ANIMALS**

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BACKGROUND OF THE INVENTION

1. Field of the Invention

The present invention relates to the cloning, expression and functional characterization of mammalian melanocortin receptor genes. The invention provides nucleic acid encoding mammalian melanocortin receptors, recombinant expression constructs comprising said nucleic acid, and mammalian cells into which said recombinant expression constructs have been introduced, and that express functional mammalian melanocortin receptors. The invention also provides a panel of such transformed mammalian cells expressing melanocortin receptors for screening compounds for receptor agonist and antagonist activity. The invention provides methods for using such panels of melanocortin receptor-expressing mammalian cells to specifically detect and identify agonists and antagonists for each melanocortin receptor, as well as patterns of agonist and antagonist activity of said compounds for the class of melanocortin receptors. Such screening methods provide a means for identifying compounds with patterns of melanocortin agonist and antagonist activity which is associated with the capacity to influence or modify physiological function and behavior, particularly metabolism and feeding behavior.

2. Background of the Invention

The proopiomelanocortin (POMC) gene product is processed to produce a large number of biologically active peptides. Two of these peptides, α -melanocyte stimulating hormone (α MSH), and adrenocorticotrophic hormone (ACTH) have well understood roles in control of melanocyte and adrenocortical function, respectively. Both of these hormones are also found in a variety of forms with unknown functions, for example, γ -melanocyte stimulating hormone (γ MSH), which has little or no ability to stimulate pigmentation (Ling *et al.*, 1979, *Life Sci.* 25: 1773-1780; Slominski *et al.*, 1992, *Life Sci.* 50: 1103-1108). A melanocortin receptor gene specific for each of the α MSH, ACTH and γ MSH hormones has been discovered by some of the present inventors (see U.S. Patent Nos. 5,280,112, 5,532,347 and U.S. Application Serial No. 08/044,812, incorporated by reference herein). In addition, two other melanocortin receptor genes

have been discovered by some of the present inventors (see Lu *et al.*, 1994, *Nature* 371: 799-802; Mountjoy *et al.*, 1994, *Molec. Endocrinol.* 8: 1298-1308) and others (see Gantz *et al.*, 1993, *J. Biol. Chem.* 268: 15174-15179 and Labbe *et al.*, 1994, *Biochem.* 33: 4543-4549).

5 Along with the well-recognized activities of α MSH in melanocytes and ACTH in adrenal and pituitary glands, the melanocortin peptides also have a diverse array of biological activities in other tissues, including the brain and immune system, and bind to specific receptors in these tissues with a distinct pharmacology (see, Hanneman *et al.*, in *Peptide Hormone as Prohormones*, G. Martinez, ed. (Ellis Horwood Ltd.: Chichester, UK) pp. 53-82; DeWied & Jolles, 1982, *Physiol. Rev.* 62: 976-1059 for reviews). A
10 complete understanding of these peptides and their diverse biological activities requires the isolation and characterization of their corresponding receptors. Some biochemical studies have been reported in the prior art.

 Shimuze, 1985, *Yale J. Biol. Med.* 58: 561-570 discusses the physiology of
15 melanocyte stimulating hormone.

 Tatro & Reichlin, 1987, *Endocrinology* 121: 1900-1907 disclose that MSH receptors are widely distributed in rodent tissues.

 Sola *et al.*, 1989, *J. Biol. Chem.* 264: 14277-14280 disclose the molecular weight characterization of mouse and human MSH receptors linked to radioactively and
20 photoaffinity labeled MSH analogues.

 Siegrist *et al.*, 1991, *J. Receptor Res.* 11: 323-331 disclose the quantification of receptors on mouse melanoma tissue by receptor autoradiography.

 Cone & Mountjoy, U.S. Patent No. 5,532,347 disclose the isolation of human and mouse α -MSH receptor genes and uses thereof (incorporated herein by reference).

25 Cone & Mountjoy, U.S. Patent No. 5,280,112 disclose the isolation of human and bovine ACTH receptor genes and uses thereof (incorporated herein by reference).

 Mountjoy *et al.*, 1992, *Science* 257: 1248-1251 disclose the isolation of cDNAs encoding mammalian ACTH and MSH receptor proteins.

 POMC neurons are present in only two regions of the brain, the arcuate nucleus
30 of the hypothalamus, and the nucleus of the solitary tract of the brain stem. Neurons from both sites project to a number of hypothalamic nuclei known to be important in feeding behavior, including the paraventricular nucleus, lateral hypothalamic area, and

ventromedial hypothalamic nucleus. While previous reports have claimed both stimulatory and inhibitory effects of α -MSH on feeding behavior (see Shimizu *et al.*, 1989, *Life Sci.* 45: 543-552; Tsujii *et al.*, 1989, *Brian Res. Bull.* 23: 165-169), knowledge of specific melanocortin receptors, their location within the central nervous system and the necessary pharmacological tools were not sufficiently developed at that time to allow the resolution of this issue. The present inventors have shown herein that a novel antagonist of the MC-3 and MC-4 melanocortin receptors can substantially increase food consumption in animals engaged in normal or fast-induced feeding behavior. This is consistent with expression of both MC-3 and MC-4 receptor mRNAs at these sites in *in situ* hybridization studies (Roselli-Rehfuss *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90: 8856-8860; Mountjoy *et al.*, 1994, *Molec. Endocrinol.* 8: 1298-1308). Moreover, the regulation of arcuate nucleus POMC gene expression is consistent with an inhibitory role for POMC in feeding behavior. POMC mRNA levels are decreased following a fast (Bergendahl *et al.*, 1992, *Neuroendocrinol.* 56: 913-920; Brady *et al.*, 1990, *Neuroendocrinol.* 52: 441-447), and a significant diurnal variation in POMC mRNA levels in the arcuate nucleus is seen in rat, with the nadir occurring around the onset of nighttime feeding at 1800 hrs (Steiner *et al.*, 1994, *FASEB J.* 8: 479-488).

Thus, the experimental evidence indicates that POMC neurons play an important role in tonic inhibition of feeding behavior, wherein obesity results from a chronic disruption of this inhibitory tone by antagonism of central melanocortin receptors in at least one animal model (*agouti*).

These results reveal for the first time a need in the art for a means for characterizing mammalian melanocortin receptor agonists and antagonists *in vitro* for the development of compounds that affect feeding behavior in animals.

SUMMARY OF THE INVENTION

The present invention provides a biological screening system for identifying and characterizing compounds that are agonists or antagonists of mammalian melanocortin receptors. The biological screening system of the invention comprises a panel of transformed mammalian cells comprising a recombinant expression construct encoding

a mammalian melanocortin receptor, and expressing said receptor thereby. The invention provides such a panel of transformed mammalian cells wherein the panel comprises cells expressing each type of mammalian melanocortin receptor. Thus, the invention also provides nucleic acid encoding mammalian melanocortin receptors, recombina⁵nt expression constructs comprising said nucleic acid, and mammalian cells into which said recombinant expression constructs have been introduced, and that express functional mammalian melanocortin receptors. Methods for using such panels of melanocortin receptor-expressing mammalian cells to specifically detect and identify agonists and antagonists for each melanocortin receptor, as well as patterns of agonist and antagonist activity of said compounds for the class of melanocortin receptors, are¹⁰ also provided. Such screening methods provide a means for identifying compounds with patterns of melanocortin agonist and antagonist activity which is associated with the capacity to influence or modify metabolism and behavior in an animal, particularly feeding behavior.

Thus, the invention provides in a first aspect a biological screening panel for determining the melanocortin receptor agonist/antagonist profile of a test compound. The panel comprises a first mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the α -MSH (MC-1) receptor. The panel also comprises a second mammalian cell comprising a recombinant²⁰ expression construct encoding a mammalian melanocortin receptor that is the ACTH (MC-2) receptor. The panel also comprises a third mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-3 receptor. The panel also comprises a fourth mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is²⁵ the MC-4 receptor. The panel also comprises a fifth mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-5 receptor. As provided by the invention, each mammalian cell expresses the melanocortin receptor encoded by the recombinant expression construct comprising said cell.

³⁰ In preferred embodiments, the melanocortin receptors encoded by the recombinant expression constructs comprising the transformed mammalian cells comprising the panel are mouse MC-1 receptor (SEQ ID Nos.: 3 and 4); human MC-1

receptor (SEQ ID Nos.: 5 and 6), human MC-2 (ACTH) receptor (SEQ ID Nos.: 7 and 8), bovine MC-2 receptor (SEQ ID Nos.: 9 and 10), rat MC-3 receptor (SEQ ID Nos.: 11 and 12), human MC-4 receptor (SEQ ID Nos.: 15 and 16) and mouse MC-5 receptor (SEQ ID Nos.: 17 and 18).

5 In a second aspect, the invention provides a method for using the melanocortin receptor panel to identify and characterize test compounds as melanocortin receptor agonists and/or antagonists. In this embodiment, the method provided by the invention identifies a melanocortin receptor agonist, and comprises the steps of contacting each of the cells of the panel with a test compound to be characterized as an agonist of a
10 mammalian melanocortin receptor and detecting binding of the test compound to each of the mammalian melanocortin receptors by assaying for a metabolite produced in the cells that bind the compound. In a preferred embodiment, the detected metabolite is cAMP.

In a preferred embodiment of this method, each of the cells of the panel of
15 mammalian cells expressing mammalian melanocortin receptors further comprises a recombinant expression construct encoding a cyclic AMP responsive element (CRE) transcription factor binding site that is operatively linked to a nucleic acid sequence encoding a protein capable of producing a detectable metabolite. In preferred embodiments, said protein is β -galactosidase, most preferably encoded by a nucleic acid
20 comprising the recombinant expression construct identified as pCRE/ β -galactosidase (as disclosed in Chen *et al.*, 1994, *Analyt. Biochem.* 226: 349-354). As provided by the invention, expression of the protein that produces the detectable metabolite is dependent on binding of the test compound to the melanocortin receptor expressed by each cell in the panel and the intracellular production of cAMP as a result. In this embodiment,
25 cAMP production results in expression of a protein capable of producing a detectable metabolite, the protein most preferably being β -galactosidase. In preferred embodiments, the detectable metabolite absorbs light to produce a colored product. Thus, this embodiment of the invention provides a panel of melanocortin receptor-expressing cells whereby melanocortin hormone binding results in the production of a
30 colored product in proportion to the extent of cAMP production in the cell as a result of hormone receptor binding.

In another embodiment of this aspect of the invention is provided a method for characterizing a compound as an antagonist of a mammalian melanocortin receptor. In this embodiment, the method comprises the steps of contacting each of the cells of the panel with an agonist of the mammalian melanocortin receptor in an amount sufficient to produce a detectable amount of a metabolite produced in the cells that bind the agonist, in the presence or absence of a test compound to be characterized as an antagonist of a mammalian melanocortin receptor, and detecting the amount of the metabolite produced in each cell in the panel in the presence of the test compound with the amount of the metabolite produced in each cell in the panel in the absence of the test compound. As provided by the assay, inhibition of the production of the detectable metabolite is used as an indication that the tested compound is a melanocortin receptor antagonist, which is further characterized quantitatively by the extent of said inhibition.

In a preferred embodiment of this method, each of the cells of the panel of mammalian cells expressing mammalian melanocortin receptors further comprises a recombinant expression construct encoding a cyclic AMP responsive element (CRE) transcription factor binding site that is operatively linked to a nucleic acid sequence encoding a protein capable of producing a detectable metabolite. In preferred embodiments, said protein is β -galactosidase, most preferably encoded by a nucleic acid comprising the recombinant expression construct identified as pCRE/ β -galactosidase. As provided by the invention, expression of the protein that produces the detectable metabolite is dependent on binding of the test compound to the melanocortin receptor expressed by each cell in the panel. In preferred embodiments, the detectable metabolite absorbs light to produce a colored product. Thus, this embodiment of the invention provides a panel of melanocortin receptor-expressing cells whereby melanocortin hormone binding results in the production of a colored product in proportion to the extent of cAMP production in the cell as a result of hormone receptor binding.

The invention also provides melanocortin receptor agonists identified by the methods and using the screening panel of the invention. In preferred embodiments, the agonist is an agonist of the MC-3 mammalian melanocortin receptor. In other preferred embodiments, the agonist is an agonist of the MC-4 mammalian melanocortin receptor.

The invention provides melanocortin receptor antagonists identified by the methods and using the screening panel of the invention. In preferred embodiments, the

antagonist is an antagonist of the MC-3 mammalian melanocortin receptor. In other preferred embodiments, the antagonist is an antagonist of the MC-4 mammalian melanocortin receptor.

5 The invention also provides methods for characterizing mammalian melanocortin receptor agonists for the capacity to modify or influence metabolism and feeding behavior in an animal. In a first aspect, the invention provides a method for characterizing melanocortin receptor MC-3 or MC-4 agonists as inhibitors of feeding behavior in an animal, the method comprising the steps of providing food to an animal that has been deprived of food for at least 12 hours, with or without administering to the
10 animal an MC-3 or MC-4 receptor agonist of the invention, and comparing the amount of food eaten by the animal after administration of the MC-3 or MC-4 receptor agonist with the amount of food eaten by the animal without administration of the MC-3 or MC-4 receptor agonist.

In another aspect, the invention provides a method for characterizing a
15 melanocortin MC-3 or MC-4 receptor antagonist as a stimulator of feeding behavior in an animal. In this embodiment, the method comprises the steps of providing food to an animal not deprived of food for at least 12 hours, with or without administering to the animal an MC-3 or MC-4 receptor antagonist, immediately prior to the onset of darkness or nighttime, and comparing the amount of food eaten by the animal after administration
20 of the MC-3 or MC-4 receptor antagonist with the amount of food eaten by the animal without administration of the MC-3 or MC-4 receptor antagonist.

Thus, the invention also provides methods for using certain of the melanocortin receptor agonists and antagonists for modifying feeding behavior in an animal. In a first aspect, the invention provides a method for stimulating feeding in an animal, the method
25 comprising administering to the animal an MC-3 or MC-4 receptor antagonist. In a preferred embodiment, the antagonists are administered systemically. In additional embodiments, the antagonists are administered intracerebroventricularly.

In another aspect, the invention provides a method for inhibiting feeding in an animal, the method comprising administering to the animal an MC-3 or MC-4 receptor
30 agonist. In a preferred embodiment, the agonists are administered systemically. In additional embodiments, the agonists are administered intracerebroventricularly.

In yet another aspect, the invention provides mammalian melanocortin receptor agonists having the general formula:



wherein A is an aliphatic amino acid residue, including for example Leu, Ile, Nle and Met, as well as analogues and substituted derivatives thereof; B is an acidic amino acid residue, including for example Asp and Glu; C is a basic amino acid residue, such as His; D is an aromatic amino acid residue having a D- conformation, including D-Phe, D-Tyr and substituted derivatives thereof; E is a basic amino acid residue, for example Arg, Lys, homoArg, homoLys, and analogues or substituted derivatives thereof; F is Trp or substituted derivatives thereof; and G is Lys, homoLys or a substituted derivative thereof. In the peptide embodiments of the melanocortin receptor agonists of the invention, the peptide is cyclized by the formation of an amide bond between the side chain carboxyl group of the Asp or Glu residue at position B in the peptide, and the side chain amino group of the Lys or homoLys residue at position G. In preferred embodiments, the melanocortin receptor agonists of the invention are agonists of the MC-3 or MC-4 receptor.

The invention also provides mammalian melanocortin receptor antagonists having the general formula:



wherein A is an aliphatic amino acid residue, including for example Leu, Ile, Nle and Met, as well as analogues and substituted derivatives thereof; B is an acidic amino acid residue, including for example Asp and Glu; C is a basic amino acid residue, such as His; D is an aromatic amino acid residue having a D- conformation, including D-Nal and substituted derivatives thereof; E is a basic amino acid residue, for example Arg, Lys, homoArg, homoLys, and analogues or substituted derivatives thereof; F is Trp or substituted derivatives thereof; and G is Lys, homoLys or a substituted derivative thereof. In the peptide embodiments of the melanocortin receptor antagonists of the invention, the peptide is cyclized by the formation of an amide bond between the side chain carboxyl group of the Asp or Glu residue at position B in the peptide, and the side chain amino group of the Lys or homoLys residue at position G. In preferred embodiments, the melanocortin receptor antagonists of the invention are agonists of the MC-3 or MC-4 receptor.

It is an advantage of the present invention that it provides an *in vitro* screening method for characterizing compounds having melanocortin receptor activities that relate to feeding behavior in animals. Specifically, the invention advantageously provides means and methods for identifying compounds having melanocortin receptor agonist and/or antagonist activity that have been associated with either stimulating or inhibiting feeding behavior when administered to an animal. The invention thus provides an economical first step in screening compounds for the capacity to affect feeding behavior, including synthetic, peptidomimetic or organomimetic derivatives of melanocortin receptor agonists or antagonists as disclosed herein or elsewhere.

Specific preferred embodiments of the present invention will become evident from the following more detailed description of certain preferred embodiments and the claims.

DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B illustrate the nucleotide (SEQ ID No.: 3) and amino acid (SEQ ID No.: 4) sequence of the mouse melanocyte stimulating hormone receptor gene.

Figures 2A and 2B illustrate the nucleotide (SEQ ID No.: 5) and amino acid (SEQ ID No.: 6) sequence of the human melanocyte stimulating hormone receptor gene.

Figures 3A and 3B illustrate the nucleotide (SEQ ID No.: 7) and amino acid (SEQ ID No.: 8) sequence of the human adrenocorticotrophic stimulating hormone receptor gene.

Figures 4A and 4B illustrate the nucleotide (SEQ ID No.: 9) and amino acid (SEQ ID No.: 10) sequence of the bovine adrenocorticotrophic stimulating hormone receptor gene.

Figures 5A and 5B illustrate the nucleotide (SEQ ID No.: 11) and amino acid (SEQ ID No.: 12) sequence of the rat melanocortin-3 receptor gene.

Figures 6A and 6B illustrate the nucleotide (SEQ ID No.: 15) and amino acid (SEQ ID No.: 16) sequence of the human melanocortin-4 receptor gene.

Figures 7A and 7B illustrate the nucleotide (SEQ ID No.: 17) and amino acid (SEQ ID No.: 18) sequence of the mouse melanocortin-5 receptor gene.

Figure 8 shows a graph of intracellular cAMP accumulation resulting from melanocyte stimulating hormone receptor agonist binding in human 293 cells transfected with a MSH receptor-encoding recombinant expression construct, wherein \square represents binding of NDP-MSH, \circ represents binding of ACTH and Δ represents binding of α MSH.

Figure 9 illustrates the cAMP response of mouse Y1 cells to binding of melanocortin peptides to human melanocortin-2 (ACTH) receptor, as measured by the β -galactosidase assay described in Example 4, wherein \blacksquare represents binding to wild-type ACTH-R and \blacktriangle represents binding to an ACTH-R variant.

Figure 10 illustrates the results of competition binding experiments of melanocortin peptides to cells expressing a recombinant expression construct encoding the rat melanocortin-3 receptor, wherein \blacksquare represents binding of NDP-MSH, \blacktriangle represents binding of γ MSH, \bullet represents binding of α MSH, \circ represents binding of ACTH₄₋₁₀ and \square represents binding of ORG2766.

Figures 11A through 11C illustrate the results of experiments showing intracellular cAMP accumulation caused by receptor-ligand binding in human 293 cells expressing the MC-3 receptor. In Figure 11A, \bullet represents binding of α MSH, \blacksquare represents binding of γ_2 -MSH, \blacktriangle represents binding of des-acetyl α MSH and \square represents binding of ACTH₁₋₃₉. In Figure 11B, \bullet represents binding of γ_1 -MSH, \blacksquare represents binding of γ_2 -MSH and \blacktriangle represents binding of des-acetyl γ -MSH. In Figure 11C, \bullet represents binding of ACTH₄₋₁₀, \blacksquare represents binding of NDP-MSH and \blacktriangle represents binding of ORG2766.

Figure 12 shows a graph of intracellular cAMP accumulation resulting from peptide binding to human melanocortin-4 receptor agonist in human 293 cells transfected with a MC-4 receptor-encoding recombinant expression construct, wherein \square represents binding of ACTH₄₋₁₀, \bullet represents binding of ACTH₁₋₃₉, \blacksquare represents binding of NDP-MSH, \circ represents binding of α MSH, Δ represents binding of γ_2 -MSH, and \blacktriangle represents binding of des-acetyl α MSH.

Figure 13 illustrates the results of cAMP accumulation and cAMP-dependent β -galactosidase assays of melanocortin peptide binding to a rat melanocortin-5 receptor, wherein \square represents binding of α MSH, Δ represents binding of β -MSH, and \circ

represents binding of γ -MSH, each determined using the β -gal method, and wherein \blacksquare - represents binding of α MSH, \blacktriangle - represents binding of β -MSH, and \bullet - represents binding of γ -MSH, each determined using the cAMP method.

Figure 14 illustrates the structure of the pCRE/ β -gal plasmid.

5 Figure 15 illustrates the results of the β -galactosidase-coupled, colorimetric melanocortin receptor binding assay using cells expressing each of the MC- 1, MC-3, MC4 or MC-5 receptors and contacted with α MSH or a variety of α MSH analogues, wherein \blacksquare - represents binding of α MSH, \blacktriangle - represents binding of NDP-MSH, \bullet - represents binding of SHU9128 (*para*-F1 substituted), \square - represents binding of SHU9203 (*p*-Cl substituted), Δ - represents binding of SHU8914 (*p*-I substituted), and \circ - represents binding of SHU9119.

Figures 16A through 16 D show the results of the β -galactosidase-coupled, colorimetric melanocortin receptor binding assay to determine antagonist activity of melanocortin analogues SHU9119 and SHU8914 in cells expressing each of the melanocortin receptors MC-3 and MC-4. In Figure 16A, \blacksquare - represents binding of α MSH, \square - represents binding of 100nM SHU9119, Δ - represents binding of 10nM SHU9119, and \circ - represents binding of 1nM SHU9119. In Figure 16B, \blacksquare - represents binding of α MSH, \square - represents binding of 100nM SHU9119, Δ - represents binding of 50nM SHU9119, and \circ - represents binding of 10nM SHU9119. In Figure 16C, \blacksquare - represents binding of α MSH, \square - represents binding of 1000nM SHU8914, Δ - represents binding of 100nM SHU8914, and \circ - represents binding of 10nM SHU8614. In Figure 16D, \blacksquare - represents binding of α MSH, \square - represents binding of 100nM SHU8914, Δ - represents binding of 50nM SHU8914, and \circ - represents binding of 10nM SHU8614.

25 Figure 17 shows the results of classic competition binding assays using the melanocortin analogues SHU9119 and SHU8914 at the MC3-R and MC-4 R receptors, wherein \blacksquare - represents binding of NDP-MSH, Δ - represents binding of SHU8914 (*p*-I substituted), and \circ - represents binding of SHU9119.

Figures 18A and 18B shows the results of cAMP accumulation experiments (performed using the β -galactosidase assay of Example 4) for rat MC-3 receptor (Figure 18A) and for mouse MC-4 receptor (Figure 18B). In Figure 18A, \blacksquare - represents

binding of NDP-MSH, -▲- represents binding of MTII and -▼- represents binding of forskolin. In Figure 18B, -■- represents binding of MTII, -▲- represents binding of NDP-MSH and -▼- represents binding of forskolin.

5 Figures 19A through 19C show the effect on food intake of intracerebroventricular administration of melanocortin analogue SHU9119 in mice. In Figure 19A, -■- represents administration of acsf (n=7) and -●- represents administration of 6nmol of SHU9119 (n=6). In Figure 19B, -■- represents administration of acsf (n=6) and -□- represents administration of 6nmol of SHU9119 (n=6). In Figure 19C, -○- represents administration of acsf (n=11) and -●- represents administration of 6nmol of SHU9119 (n=12).
10

 Figures 20A through 20C show the effect on food intake of intracerebroventricular administration of melanocortin analogue MTII in mice. In Figure 20A, -●- represents administration of acsf (n=8), -▼- represents administration of 0.1nmol MTII (n=8), -■- represents administration of 1nmol MTII (n=7) and -▲- represents administration of 3nmol MTII (n=9). In Figure 20B, -●- represents administration of acsf (n=12), -□- represents administration of 3nmol MTII and 6nmol SHU9119 (n=9) and -▲- represents administration of 3nmol MTII (n=9).
15

 Figure 20D shows the effect on locomotor activity of intracerebroventricular administration of melanocortin analogue MTII in mice, wherein -■- represents administration of vehicle alone (n=6) and -▲- represents administration of 3nmol MTII (n=6).
20

 Figures 21A through 21D show the effect on food intake of intracerebroventricular administration of melanocortin analogue MTII in mice. In Figure 21A, -●- represents administration of acsf (n=6) and -▲- represents administration of 3nmol MTII (n=7). In Figure 21B, open bars represent administration of acsf (n=6), solid bars represents administration of 1.18nmol neuropeptide Y (NPY; n=6) and stipled bars represents administration of 3nmol MTII and 1.18nmol NPY (n=6). In Figure 21C, -●- represents administration of acsf (n=7) and -▲- represents administration of 3nmol MTII (n=7). In Figure 21D, -■- represents administration of 100nmol MTII (n=6) and -▲- represents administration of vehicle alone (n=6).
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DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

The term "melanocortin receptor" as used herein reference to proteins having the biological activity of any of the disclosed melanocortin receptors, including the MC-1 (SEQ ID Nos.: 3, 4, 5 and 6), MC-2 (ACTH; SEQ ID Nos.: 7, 8, 9 and 10), MC-3 (SEQ ID Nos.: 11 and 12), MC-4 (SEQ ID Nos.: 15 and 16) or MC-5 (SEQ ID Nos.: 17 and 18) receptors, as well as naturally-occurring and genetically-engineered allelic variations in these sequences.

Cloned nucleic acid provided by the present invention may encode MC receptor protein of any species of origin, including, for example, mouse, rat, rabbit, cat, and human, but preferably the nucleic acid provided by the invention encodes MC receptors of mammalian, most preferably rodent and human, origin.

The production of proteins such as the MC receptors from cloned genes by genetic engineering means is well known in this art. The discussion which follows is accordingly intended as an overview of this field, and is not intended to reflect the full state of the art.

DNA which encodes MC receptors may be obtained, in view of the instant disclosure, by chemical synthesis, by screening reverse transcripts of mRNA from appropriate cells or cell line cultures, by screening genomic libraries from appropriate cells, or by combinations of these procedures, as illustrated below. Screening of mRNA or genomic DNA may be carried out with oligonucleotide probes generated from the MC receptor gene sequence information provided herein. Probes may be labeled with a detectable group such as a fluorescent group, a radioactive atom or a chemiluminescent group in accordance with know procedures and used in conventional hybridization assays, as described in greater detail in the Examples below. In the alternative, MC receptor gene sequences may be obtained by use of the polymerase chain reaction (PCR) procedure, with the PCR oligonucleotide primers being produced from the MC receptor gene sequences provided herein. See U.S. Patent Nos. 4,683,195 to Mullis *et al.* and 4,683,202 to Mullis.

MC receptor proteins may be synthesized in host cells transformed with a recombinant expression construct comprising a nucleic acid encoding each of the receptors disclosed herein. Such a recombinant expression construct can also be comprised of a vector that is a replicable DNA construct. Vectors are used herein either

to amplify DNA encoding an MC receptor and/or to express DNA which encodes an MC receptor. For the purposes of this invention, a recombinant expression construct is a replicable DNA construct in which a DNA sequence encoding an MC receptor is operably linked to suitable control sequences capable of effecting the expression of the receptor in a suitable host cell. The need for such control sequences will vary depending upon the host selected and the transformation method chosen. Generally, control sequences include a transcriptional promoter, an optional operator sequence to control transcription, a sequence encoding suitable mRNA ribosomal binding sites, and sequences which control the termination of transcription and translation. Amplification vectors do not require expression control domains. All that is needed is the ability to replicate in a host, usually conferred by an origin of replication, and a selection gene to facilitate recognition of transformants. *See, Sambrook et al., 1990, Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Press: New York).

Also specifically provided by the invention are reporter expression constructs comprising a nucleic acid encoding a protein capable of expressing a detectable phenotype, such as the production of a detectable reporter molecule, in a cell expressing the construct. Such constructs can be used for producing recombinant mammalian cell lines in which the reporter construct is stably expressed. Most preferably, however, the reporter construct is provided and used to induce transient expression over an experimental period of from about 18 to 96 hrs in which detection of the reporter protein-produced detectable metabolite comprises an assay. Such reporter expression constructs are also provided wherein induction of expression of the reporter construct is controlled by a responsive element operatively linked to the coding sequence of the reporter protein, so that expression is induced only upon proper stimulation of the responsive element. Exemplary of such a responsive element is a cAMP responsive element (CRE), which induces expression of the reporter protein as a result of an increase in intracellular cAMP concentration. In the context of the present invention, such a stimulus is associated with melanocortin receptor binding, so that a reporter construct comprising one or more CREs is induced to express the reporter protein upon binding of a receptor agonist to a MC receptor in a recombinantly transformed mammalian cell. Production and use of such a reporter construct is illustrated below in Example 5.

Vectors useful for practicing the present invention include plasmids, viruses (including phage), retroviruses, and integratable DNA fragments (*i.e.*, fragments integratable into the host genome by homologous recombination). The vector replicates and functions independently of the host genome, or may, in some instances, integrate into the genome itself. Suitable vectors will contain replicon and control sequences which are derived from species compatible with the intended expression host. A preferred vector is the plasmid pcDNA/neo I. Transformed host cells are cells which have been transformed or transfected with recombinant expression constructs made using recombinant DNA techniques and comprising mammalian MC receptor-encoding sequences. Preferred host cells are human 293 cells. Preferred host cells for the MC-2 (ACTH) receptor are Y1 cells (subclone OS3 or Y6). Transformed host cells are chosen that ordinarily express functional MC receptor protein introduced using the recombinant expression construct. When expressed, the mammalian MC receptor protein will typically be located in the host cell membrane. *See, Sambrook et al., ibid.*

Cultures of cells derived from multicellular organisms are a desirable host for recombinant MC receptor protein synthesis. In principal, any higher eukaryotic cell culture is workable, whether from vertebrate or invertebrate culture. However, mammalian cells are preferred, as illustrated in the Examples. Propagation of such cells in cell culture has become a routine procedure. *See Tissue Culture*, Academic Press, Kruse & Patterson, editors (1973). Examples of useful host cell lines are human 293 cells, VERO and HeLa cells, Chinese hamster ovary (CHO) cell lines, mouse Y1 (subclone OS3), and WI138, BHK, COS-7, CV, and MDCK cell lines. Human 293 cells are preferred.

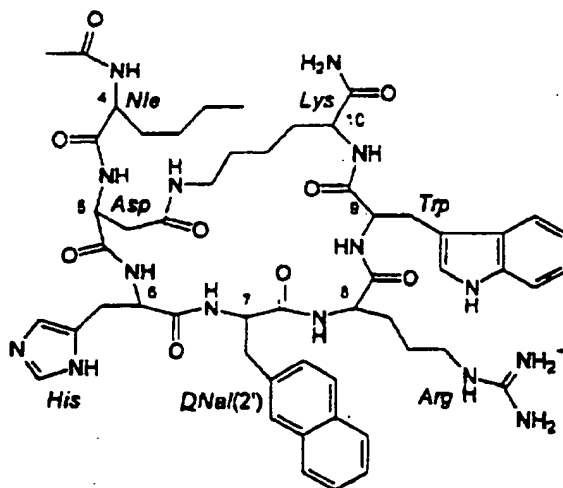
Cells expressing mammalian MC receptor proteins made from cloned genes in accordance with the present invention may be used for screening agonist and antagonist compounds for MC receptor activity. Competitive binding assays are well known in the art and are described in the Examples below. Such assays are useful for drug screening of MC receptor agonist and antagonist compounds, as detected in receptor binding assays as described below.

One particular use of such screening assays are for developing drugs and other compounds useful in modifying or changing feeding behavior in mammals. The invention provides an assay system, comprising a panel of recombinant mammalian

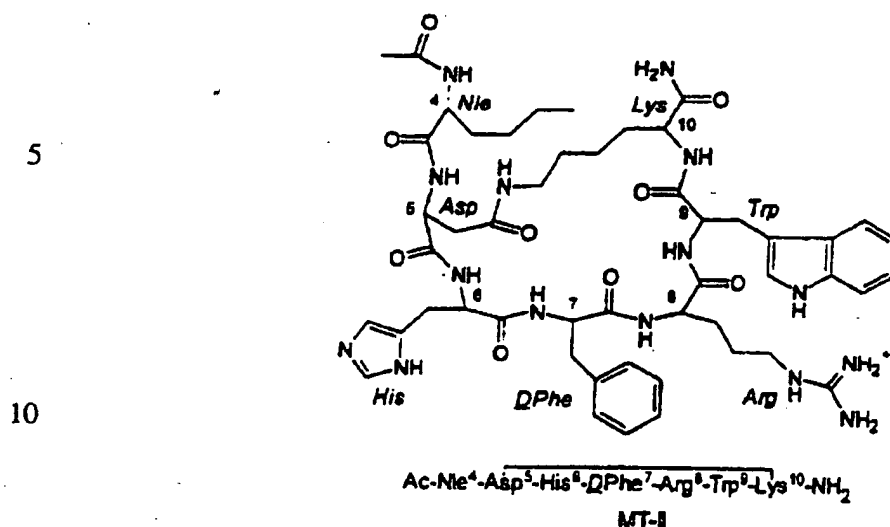
cells, heterologously expressing each of the MC receptors disclosed herein, wherein the panel is constructed of at least one cell line expressing an MC receptor, and most preferably comprising cells expressing each of the MC receptors. The invention provides such panels also comprising a detection means for detecting receptor agonist or antagonist binding, such as the reporter expression constructs described herein, using direct binding and competition binding assays as described in the Examples below. In the use of this panel, each MC receptor is assayed for agonist or antagonist patterns of binding a test compound, and a characteristic pattern of binding for all MC receptors is thereby determined for each test compound. This pattern is then compared with known MC receptor agonists and antagonists to identify new compounds having a pattern of receptor binding activity associated with a particular behavioral or physiological effect.

For example, provided herein is experimental evidence that MC-3 or MC-4 receptor antagonists are capable of stimulating feeding in hungry animals, and that MC-3 or MC-4 agonists are capable of inhibiting feeding in animals otherwise stimulated to eat. The invention provides an *in vitro* assay to characterize MC-3 and MC-4 agonists/antagonists as a preliminary and economical step towards developing feeding behavior-modulating drugs for use *in vivo*.

These results on feeding behavior *in vivo* have been obtained with certain MC receptor binding analogues, SHU9119 and MTII. These compounds have the following chemical structure:



Ac-Nle¹-Asp⁵-His⁶-DNa(2')⁷-Arg⁸-Trp⁹-Lys¹⁰-NH₂
SHU-8119



15 Generally, those skilled in the art will recognize that peptides as described herein may be modified by a variety of chemical techniques to produce compounds having essentially the same activity as the unmodified peptide, and optionally having other desirable properties. For example, carboxylic acid groups of the peptide, whether carboxyl-terminal or sidechain, may be provided in the form of a salt of a pharmaceutically-acceptable cation or esterified to form a C₁-C₁₆ ester, or converted to an amide of formula NR₁R₂ wherein R₁ and R₂ are each independently H or C₁-C₁₆ alkyl, or combined to form a heterocyclic ring, such as 5- or 6-membered. Amino groups of the peptide, whether amino-terminal or sidechain, may be in the form of a pharmaceutically-acceptable acid addition salt, such as the HCl, HBr, acetic, benzoic, toluene sulfonic, maleic, tartaric and other organic salts, or may be modified to C₁-C₁₆ alkyl or dialkyl amino or further converted to an amide. Hydroxyl groups of the peptide sidechain may be converted to C₁-C₁₆ alkoxy or to a C₁-C₁₆ ester using well-recognized techniques. Phenyl and phenolic rings of the peptide sidechain may be substituted with one or more halogen atoms, such as fluorine, chlorine, bromine or iodine, or with C₁-C₁₆ alkyl, C₁-C₁₆ alkoxy, carboxylic acids and esters thereof, or amides of such carboxylic acids. Methylene groups of the peptide sidechains can be extended to homologous C₂-C₄ alkylenes. Thiols can be protected with any one of a

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number of well-recognized protecting groups, such as acetamide groups. Those skilled in the art will also recognize methods for introducing cyclic structures into the peptides of this invention to select and provide conformational constraints to the structure that result in enhanced binding and/or stability. For example, a carboxyl-terminal or amino-terminal cysteine residue can be added to the peptide, so that when oxidized the peptide will contain a disulfide bond, thereby generating a cyclic peptide. Other peptide cyclizing methods include the formation of thioethers and carboxyl- and amino-terminal amides and esters.

Peptidomimetic and organomimetic embodiments are also hereby explicitly declared to be within the scope of the present invention, whereby the three-dimensional arrangement of the chemical constituents of such peptido- and organomimetics mimic the three-dimensional arrangement of the peptide backbone and component amino acid sidechains in the peptide, resulting in such peptido- and organomimetics of the peptides of this invention having substantial biological activity.

It is implied that a pharmacophore exists for the receptor agonist and antagonist properties of these and related MC receptor binding analogues. A pharmacophore is an idealized, three-dimensional definition of the structural requirements for biological activity. Peptido- and organomimetics can be designed to fit each pharmacophore with current computer modeling software (computer aided drug design). MC receptor binding analogues derived using such software and comprising peptido- and organomimetics of SHU9119 and MTII and related analogues are within the scope of the claimed invention.

The MC receptor binding analogues, in particular those analogues that are MC-3 or MC-4 receptor agonists or antagonists are provided to be used in methods of influencing, modifying or changing feeding behavior in mammals *in vivo*. Specific examples of uses for the MC receptor binding analogues of the invention include but are not limited to treatment of eating disorders such as anorexia and obesity, and other pathological weight and eating-related disorders. Other examples are failure to thrive disorders and disease-related cachexia, such as occurs in cancer patients. Also within the scope of the analogues of the invention is use for enhancing appearance, athletic ability, or adjuvant to other therapies to treat disorders such as high blood pressure, high

serum cholesterol, vascular and heart disease, stroke, kidney disease, diabetes and other metabolic disorders.

The Examples which follow are illustrative of specific embodiments of the invention, and various uses thereof. They set forth for explanatory purposes only, and are not to be taken as limiting the invention.

EXAMPLE 1

Isolation of an α MSH Receptor Probe by Random PCR Amplification of Human Melanoma cDNA Using Degenerate Oligonucleotide Primers

In order to clone novel G-protein coupled receptors, cDNA prepared from RNA from human melanoma cells was used as template for a polymerase chain reaction (PCR)-based random cloning experiment. PCR was performed using a pair of degenerate oligonucleotide primers corresponding to the putative third and sixth transmembrane regions of G-protein coupled receptors (Libert *et al.*, 1989, *Science* 244: 569-72; Zhou *et al.*, 1990, *Nature* 347: 76-80). The PCR products obtained in this experiment were characterized by nucleotide sequencing. Two novel sequences representing novel G-protein-coupled receptors were identified.

PCR amplification was performed as follows. Total RNA was isolated from a human melanoma tumor sample by the guanidinium thiocyanate method (Chirgwin *et al.*, 1979, *Biochemistry* 18: 5294-5299). Double-stranded cDNA was synthesized from total RNA with murine reverse transcriptase (BRL, Gaithersburg, MD) by oligo-dT priming (Sambrook *et al.*, *ibid.*). The melanoma cDNA mixture was then subjected to 45 cycles of PCR amplification using 500 picomoles of degenerate oligonucleotide primers having the following sequence:

Primer III (sense):

GAGTCGACCTGTG(C/T)G(C/T)(C/G)AT(C/T)(A/G)CIIT(G/T)GAC(C/A)G(C/G)TAC
(SEQ ID NO:1)

and

Primer VI (antisense):

CAGAATTCAG(T/A)AGGGCAICCGAGCAGAI(G/C)(G/A)(T/C)GAA
(SEQ ID NO:2)

in 100 μ l of a solution containing 50 mM Tris-HCl (pH 8.3), 2.5 mM $MgCl_2$, 0.01% gelatin, 200 μ M each dNTP, and 2.5 units of *Taq* polymerase (Saiki *et al.*, 1988, *Science* 239: 487-491). These primers were commercially synthesized by Research Genetics Inc. (Huntsville, AL). Each PCR amplification cycle consisted of incubations
5 at 94°C for 1 min (denaturation), 45 C for 2 min (annealing), and 72 C for 2 min (extension).

Amplified products of the PCR reaction were extracted with phenol/chloroform and precipitated with ethanol. After digestion with *Eco*RI and *Sa*II, the PCR products were separated on a 1.2% agarose gel. A slice of this gel, corresponding to PCR
10 products of 300 basepairs (bp) in size, was cut out and purified using glass beads and sodium iodide, and the insert was then cloned into a pBKS cloning vector (Stratagene, LaJolla, CA).

A total of 172 of such pBKS clones containing inserts were sequenced using Sequenase (U.S. Biochemical Corp., Cleveland, OH) by the dideoxynucleotide chain
15 termination method (Sanger *et al.*, 1977, *Proc. Natl. Acad. Sci. USA* 74: 5463-5467). Two types of sequences homologous to other G-protein coupled receptors were identified.

EXAMPLE 2A

Isolation of a Mouse α MSH (MC-1) Receptor cDNA

Probes isolated in Example 1 was used to screen a Cloudman melanoma cDNA library in order to isolate a full-length cDNA corresponding to the cloned probe. One clone was isolated from a library of 5×10^6 clones screened as described below in Example 2B. This clone contained an insert of 2.6 kilobases (kb). The nucleotide
25 sequence of the complete coding region was determined (*see* co-owned U.S. Patent No. 5,532,347, incorporated by reference); a portion of this cDNA comprising the coding region was sequenced and is shown in Figures 1A and 1B (SEQ ID Nos: 3 & 4).

EXAMPLE 2B

Isolation of a Human α MSH (MC-1) Receptor cDNA

In order to isolate a human counterpart of the murine melanocyte α MSH receptor gene disclosed in Example 2A and co-owned U.S. Patent No. 5,532,347, a

human genomic library was screened at high stringency (50% formamide, 42°C) using the human PCR fragments isolated as described in Example 1. A genomic clone was determined to encode an human MSH receptor (SEQ ID NO:5). The human MSH receptor has a predicted amino acid sequence (SEQ ID NO:6) that is 75% identical and colinear with the mouse α MSH receptor cDNA sequence (Figures 2A and 2B, represented as human MSH-R). The predicted molecular weight of the human MSH^R is 34.7kD.

EXAMPLE 2C

Isolation of a Human ACTH (MC-2) Receptor cDNA

For cloning the ACTH receptor (MC-2), a human genomic library was screened at high stringency (50% formamide, 1M NaCl, 50nM Tris-HCl, pH 7.5, 0.1% sodium pyrophosphate, 0.2% sodium dodecyl sulfate, 100 μ g/ml salmon sperm DNA, 10X Denhardt's solution, 42°C), using the human PCR fragments isolated as described in Example 1 herein and U.S. Patent No. 5,280,112, incorporated by reference. A genomic clone was isolated that encodes a highly related G-coupled receptor protein (SEQ ID NO:7 and Figures 3A and 3B). The predicted amino acid sequence (SEQ ID NO:8) of this clone is 39% identical and also colinear, excluding the third intracellular loop and carboxy-terminal tail, with the human MSH receptor gene product. The predicted molecular weight of this putative ACTH^R is 33.9 kilodaltons (kD). This clone was identified as encoding an MC-2 receptor based on its high degree of homology to the murine and human MSH receptors, and the pattern of expression in different tissue types, as described in Example 3 in U.S. Patent 5,280,112.

EXAMPLE 2D

Isolation of a Bovine ACTH (MC-2) Receptor cDNA

A bovine genomic DNA clone encoding the bovine counterpart of the MC-2 (ACTH) receptor was isolated from a bovine genomic library, essentially as described in Example 2C above, and its nucleotide sequence determined (as shown in Figures 4A and 4B; SEQ ID Nos:9 & 10).

EXAMPLE 2E**Isolation of a Rat γ -MSH (MC-3) Receptor cDNA**

The mouse α MSH receptor cDNA isolated as described in Example 2A and co-owned U.S. Patent No. 5,532,347 was used to screen a rat hypothalamus cDNA library at low stringency (30% formamide, 5X SSC, 0.1% sodium pyrophosphate, 0.2% sodium dodecyl sulfate, 100 μ g/ml salmon sperm DNA, and 10% Denhardt's solution) at 42°C for 18h. A 1 kb cDNA clone was isolated and sequenced as described in co-owned U.S. Patent No. 5,532,347, and this clone used to re-screen the rat hypothalamus cDNA library at high stringency (same conditions as above except that formamide was present at 45%). A cDNA clone approximately 2.0 kb in length was isolated and analyzed as described in co-pending U.S. Application Serial No. 08/044,812, incorporated by reference; a portion of this cDNA comprising the coding region was sequenced and is shown in Figures 5A and 5B (SEQ ID Nos:11 & 12).

EXAMPLE 2F**Isolation of a Human MC-4 Receptor DNA**

For cloning the MC-4 receptor, a human genomic library was screened at moderate stringency (40% formamide, 1M NaCl, 50mM Tris-HCl, pH 7.5, 0.1% sodium pyrophosphate, 0.2% sodium dodecyl sulfate, 100 μ g/ml salmon sperm DNA, 10X Denhardt's solution, 42°C), using rat PCR fragments isolated as described in Example 1 herein, with the exception that the following primers were used for PCR: Primer II (sense):

GAGTCGACC(A/G)CCCATGTA(C/T)T(AGT)(C/T)TTCATCTG
(SEQ ID NO:13)

and

Primer VII (antisense):

CAGAATTTCGGAA(A/G)GC(A/G)TA(G/T)ATGA(A/G)GGGGTC
(SEQ ID NO:14)

A genomic clone was isolated that encodes a highly related G-coupled receptor protein (SEQ ID NO:15 and Figures 6A and 6B) on a 1.9kb *Hind*III fragment. The predicted amino acid sequence (SEQ ID NO:16) of this clone is 55-61% sequence

identity with human MC-3 and MC-5 receptors, and 46-47% sequence identity with the human MC-1 and MC-2 (ACTH) receptor.

EXAMPLE 2G

Isolation of a Mouse MC-5 Receptor DNA

One million clones from a mouse 129SVJ genomic library comprising 5,000,000 clones in the λ FixII vector (Stratagene) was screened at low stringency (hybridization in 40% formamide at 42°C, washing performed in 0.5X SSC at 60°C, as described above in Example 2E) using radiolabeled probed from the rat MC-3 and MC-4 receptors (as described in Examples 2E and 2F). Positively-hybridizing clones were isolated and sequenced, and the sequences obtained were compared to previously-isolated melanocortin receptor clones. One clone, comprising a previously-unknown sequence, was determined to encode the MC-5 melanocortin receptor. The nucleotide and amino acid sequences of this receptor are shown in Figures 7A and 7B (SEQ ID No.: 17 & 18).

EXAMPLE 3

Construction of a Recombinant Expression Construct, DNA Transfection and Functional Expression of the MCR Gene Products

In order to produce recombinant mammalian cells expressing each of the melanocortin receptors of Example 2, cDNA from each receptor was cloned into a mammalian expression construct, the resulting recombinant expression construct transfected into human 293 cells, and cell lines generated that expressed the melanocortin receptor proteins in cellular membranes at the cell surface.

The mouse α MSH receptor was cloned by excising the entire coding region of the α MSH^R (MC-1) cDNA insert comprising a 2.1kb fragment and subcloning this fragment into the *Bam*HI/*Xho*I sites of pcDNAI/neo expression vector (Invitrogen, San Diego, CA). The resulting plasmid was prepared in large-scale through one cycle of CsCl gradient ultracentrifugation, and 20 μ g of the plasmid transfected into each 100mm dish of 293 cells using the calcium phosphate method (*see* Chen & Okayama, 1987, *l.* 7: 2745-2752). After transfection, cells were cultured in DMEM media supplemented with 10% calf serum in a 3% CO₂ atmosphere at 37°C. Selection was

performed with neomycin (G418; GIBCO) at a concentration of 1000 $\mu\text{g/ml}$; selection was started 72 hr after transfection and continued for 3 weeks.

The αMSH^R is known to couple to G-proteins and thereby activate adenylyl cyclase, increasing intracellular levels of cAMP (see Buckley & Ramachandran, 1981, *Proc. Natl. Acad. Sci. USA* 78: 7431-7435; Grahame-Smith *et al.*, 1967, *J. Biol. Chem.* 242: 5535-5541; Mertz & Catt, 1991, *Proc. Natl. Acad. Sci. USA* 88: 8525-8529; Pawalek *et al.*, 1976, *Invest. Dermatol.* 66: 200-209). This property of cells expressing the αMSH receptor was used to analyze expression of the αMSH receptor in cell colonies transfected with the expression vectors described herein as follows. Cells ($\sim 1 \times 10^6$) were plated in 6-well dishes, washed once with DMEM containing 1% bovine serum albumin (BSA) and 0.5mM IBMX (a phosphodiesterase inhibitor), then incubated for 45 minutes at 37°C with varying concentrations of the melanotropic peptides αMSH , βMSH , γMSH , the MSH peptide analogues Nle⁴, D-Phe⁷- αMSH (NDP-MSH), and ACTH. Following hormone treatment, the cells were washed twice with phosphate buffered saline and intracellular cAMP extracted by lysing the cells with 1ml of 60% ethanol. Intracellular cAMP concentrations were determined using an assay (Amersham) which measures the ability of cAMP to displace [8-³H] cAMP from a high affinity cAMP binding protein (see Gilman, 1970, *Proc. Natl. Acad. Sci. USA* 67: 305-312).

The results of these experiments are shown in Figure 8. The abscissa indicates the concentration of each hormone and the ordinate indicates the percentage of basal intracellular cAMP concentration achieved by each treatment. Points indicate the mean of duplicate incubations; the standard error did not exceed 15% for any data point. None of the peptides tested induced any change in intracellular cAMP in cells containing the vector alone. Cells expressing the murine αMSH receptor responded to melanotropic peptides with a 2-3 fold elevation of intracellular cAMP, similar to levels of cAMP induced by these peptides in the Cloudman cell line (see Pawalek, 1985, *Yale J. Biol. Med.* 58: 571-578). The EC_{50} values determined for αMSH ($2.0 \times 10^{-9}\text{M}$), ACTH ($8.0 \times 10^{-9}\text{M}$) and the superpotent MSH analogue NDP-MSH ($2.8 \times 10^{-11}\text{M}$) correspond closely to reported values (see Tatro *et al.*, 1990, *Cancer Res.* 50: 1237-1242). As expected, the βMSH peptide had an EC_{50} value comparable

to α MSH, while γ MSH had little or no activity (see Slominski *et al.*, 1992, *Life Sci.* 50: 1103-1108), confirming the identity of this receptor as a melanocyte α MSH receptor.

5 A similar series of experiments were performed using mouse Y1 cells (subclone OS3; Schimmer *et al.*, 1995, *J. Cell. Physiol.* 163: 164-171) expressing the human and bovine MC-2 (ACTH) receptor clones of Examples 2C and 2D. These results are shown in Figure 9, where the extent of cAMP responsive element-linked β -galactosidase activity (see Example 4, below) is shown with increasing concentrations of ACTH.

10 The entire coding region of the MC-3 receptor cDNA insert, obtained as described above in the co-pending U.S. Serial No. 08/044,812, was contained in a 2.0kb restriction enzyme digestion fragment and was cloned into the *Bam*HI/*Xho*I sites of pcDNA/neo I expression vector (Invitrogen, San Diego, CA). The resulting plasmid was prepared in large-scale through one cycle of CsCl gradient ultracentrifugation and 20 μ g pcDNA/MC-3 receptor DNA were transfected into each 100 mm dish of 293 cells using
15 the calcium phosphate method (see Chen & Okayama, 1987, *Mol. Cell. Biol.* 7: 2745-2752). After transfection, cells were cultured in DMEM media supplemented with 10% calf serum in a 3% CO₂ atmosphere at 37°C. Selection was performed with neomycin (G418; GIBCO) at a concentration of 1000 μ g/ml; selection was started 72 h after
20 transfection and continued for 3 weeks.

Specific binding of melanocortin peptides to cells expressing the MC-3 receptor was demonstrated by competition experiments using ¹²⁵I-labeled Nle⁴-D-Phe⁷- α -MSH (NDP-MSH, as described in Tatro *et al.*, 1990, *Cancer Res.* 50: 1237-1242). Suspended cells (2x10⁵) were incubated at 37°C with 500,000 cpm of labeled peptide for 10 min in
25 binding buffer (Ham's F10 media plus 10mM HEPES, pH 7.2, 0.25% bovine serum albumin, 500K IU/ml aprotinin, 100 μ g/ml bacitracin and 1mM 1,10-phenanthroline) in the presence or absence of the indicated concentrations of peptides. Maximum labeling was achieved within 10 min.

The results of these experiments are shown in Figure 10. Labeled NDP-MSH
30 binding to cells expressing the MC-3 receptor, produced as described above, is inhibited by competition with unlabeled peptides known to be melanocortin receptor agonists, having a relative order of potency as follows:

NDP-MSH > γ -MSH > α -MSH > ACTH₄₋₁₀ >>> ORG2766.

Approximate K_i values derived from this experiment are as shown in Table I:

TABLE I

Agonist	K _i (approx)
NDP-MSH	2 x 10 ⁻⁸
γ -MSH	5 x 10 ⁻⁸
α -MSH	1 x 10 ⁻⁷
ACTH ₄₋₁₀	8 x 10 ⁻⁵

cAMP production assays as described above were also used to analyze expression of MC3-R in cells transfected with the expression vectors described herein as follows. Cells (~5x10⁶) were plated in 6-well dishes, washed once with DMEM containing 1% bovine serum albumin (BSA) and 0.5mM IBMX (a phosphodiesterase inhibitor), then incubated for 1h at 37°C with varying concentrations of the melanotropic peptides α MSH, γ_3 MSH, γ MSH, the MSH peptide analogues Nle⁴-D-Phe⁷- α MSH (NDP-MSH), ACTH₄₋₁₀ and ACTH₁₋₃₉. Following hormone treatment, the cells were washed twice with phosphate buffered saline and intracellular cAMP extracted by lysing the cells with 1ml of 60% ethanol. Intracellular cAMP concentrations were determined using an assay which measures the ability of cAMP to displace [8-³H] cAMP from a high affinity cAMP binding protein (*see* Gilman, 1979, *Proc. Natl. Acad. Sci. USA* 67: 305-312).

The results of these experiments are shown in Figures 11A through 11C. The abscissa indicates the concentration of each hormone and the ordinate indicates the percentage of basal intracellular cAMP concentration achieved by each treatment. Points indicate the mean of duplicate incubations; the standard error did not exceed 15% for any data point. Figure 11A depicts the results of experiments using peptides found *in vivo*; Figure 11B depicts results found with γ -MSH variants; and Figure 11C shows results of synthetic melanocortin analogues. None of the peptides tested induced any change in intracellular cAMP in cells containing the vector alone. Cells expressing rat MC3-R responded strongly to every melanotropic peptide containing the MSH sequence

His-Phe-Arg-Trp, with up to a 60-fold elevation of intracellular cAMP levels. EC_{50} values ranged from 1-50 nM. The most potent ligand and the one having the lowest EC_{50} was found to be γ MSH. The order of potency for the naturally occurring melanocortins was found to be:

- 5 γ_2 -MSH = γ MSH > α MSH = ACTH₁₋₃₉ > γ_3 -MSH > *des*-acetyl- α MSH > ACTH₄₋₁₀.
 EC_{50} values for these compounds are shown in Table II:

TABLE II

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Agonist	EC_{50}
NDP-MSH	1×10^{-9}
γ_1 -MSH	3×10^{-9}
γ_2 -MSH	3×10^{-9}
α -MSH	4×10^{-9}
15 ACTH ₁₋₃₉	4×10^{-9}
γ_3 -MSH	6×10^{-9}
<i>des</i> acetyl- α MSH	8×10^{-9}
ACTH ₄₋₁₀	1×10^{-7}

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Additionally, a synthetic melanocortin peptide (ORG2766), known to have the greatest activity *in vivo* in stimulation of retention of learned behavior and in stimulation of neural regeneration, was unable to stimulate MC3-R-mediated cAMP production, and was also inactive as an antagonist. The results strongly indicate that this peptide does not bind to MC3-R protein.

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The MC-4 receptor was cloned in a 1.9kb *Hind*III genomic DNA fragment after PCR amplification of a lambda phage clone into pcDNAI/Neo (Invitrogen). This plasmid was stably introduced into human 293 cells by calcium phosphate co-precipitation using standard techniques, and plasmid-containing cells selected in G418 containing media. Specificity of receptor-hormone binding was assayed using adenylate cyclase activity as described above. The MC-4 receptor was found to couple to

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adenylate cyclase activity having the following pattern of agonist affinity:
 NDP-MSH > *des*-acetyl- α -MSH >= ACTH₁₋₃₉ >= α -MSH > γ_2 -MSH = ACTH₄₋₁₀

whereas the synthetic ACTH_{4,9} analogue ORG2766 showed no detectable binding to the MC-4 receptor. The results of adenylate cyclase activity assays are shown in Figure 12. EC₅₀ values for each of the tested MC-4 receptor agonists are as shown in Table III:

TABLE III

Agonist	EC ₅₀
NDP-MSH	1.1 x 10 ⁻¹¹ M
desacetyl- α MSH	4.9 x 10 ⁻¹⁰ M
ACTH ₁₋₃₉	6.8 x 10 ⁻¹⁰ M
α -MSH	1.5 x 10 ⁻⁹ M
γ ₂ -MSH	> 10 ⁻⁷ M
ACTH ₄₋₁₀	> 10 ⁻⁷

A 1.6kb *ApaI-HindIII* fragment comprising the entire coding sequence of the mouse MC-5 melanocortin receptor disclosed in Example 2G above was cloned into the pcDNA/neo expression vector (Invitrogen) after PCR amplification of the lambda phage clone. This plasmid was stably introduced into human 293 cells by calcium phosphate co-precipitation using standard techniques, and plasmid-containing cells selected in G418 containing media. Specificity of receptor-hormone binding was assayed using adenylate cyclase activity as described above. The MC-5 receptor was found to couple to adenylate cyclase activity having the following pattern of agonist affinity:

$$\alpha\text{-MSH} > \beta\text{MSH} > \gamma\text{-MSH}$$

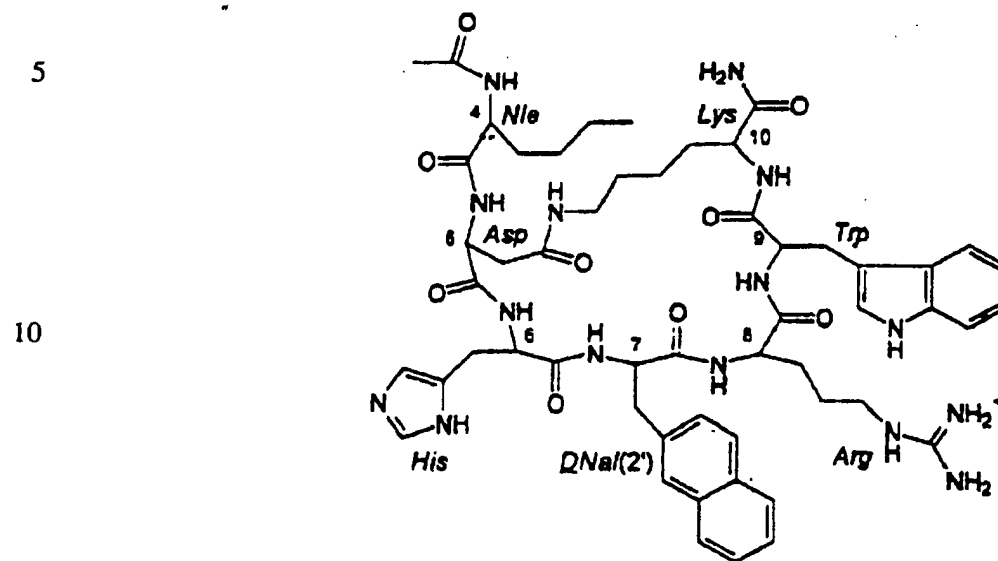
The results of adenylate cyclase activity assays are shown in Figure 13. EC₅₀ values for each of the tested MC-5 receptor agonists are: α -MSH=1.7 x 10⁻⁹M; and β MSH = 5 x 10⁻⁹M.

EXAMPLE 4

Melanocortin Analogue Binding to Mammalian Melanocortin Receptors

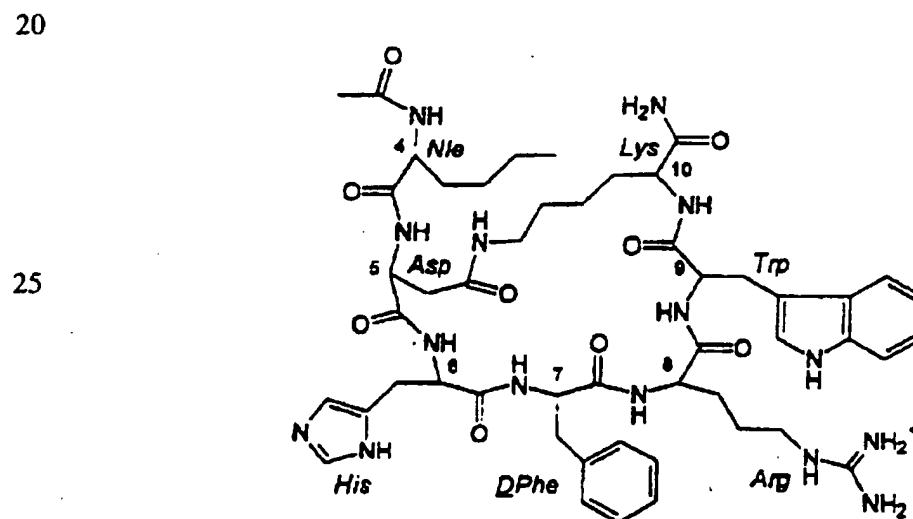
Recombinant cells prepared as described above in Example 3 were used to characterize receptor binding of two melanocortin analogues comprising cyclic lactam heptapeptides.

The melanocortin receptor analogue SHU9119 has the following chemical structure:



Ac-Nle⁴-cyclo(Asp⁵, D-Nal(2')⁷, Lys¹⁰) αMSH-(4-10)-amide

The melanocortin receptor analogue MTII has the following chemical structure:



Ac-Nle⁴-cyclo(Asp⁵, His⁶, D-Phe⁷, Arg⁸, Trp⁹, Lys¹⁰) αMSH-(4-10)-amide

These analogues were prepared as described in Hruby *et al.* (1995, *J. Med. Chem.* 38: 3454-3461).

These analogues were tested for melanocortin receptor binding using a colorimetric assay system developed by some of the instant inventors (Chen *et al.*, 1995, *Analyt. Biochem.* 226: 349-354) as follows. A series of concatamers of the synthetic oligonucleotide:

5'-GAATTCGACGTCACAGTATGACGGCCATGG-3'
(SEQ ID No:19)

was produced by self-annealing and ligation and a tandem tetramer obtained. This fragment was cloned upstream of a fragment of the human vasoactive intestinal peptide (-93-+152; SEQ ID No.: 13; see Fink *et al.*, 1988, *Proc. Natl. Acad. Sci. USA* 85: 6662-6666). This promoter was then cloned upstream of the β -galactosidase gene from *E. coli*. The resulting plasmid construct is shown in Figure 14.

Transient transfection of the pCRE/ β -gal plasmid described above was performed as follows. Cells grown to between 40-60% confluency (corresponding to about 1.5 million cells/6cm tissue culture plate) were incubated with Opti-MEM (GIBCO-BRL, Long Island, NY) and then contacted with a pCRE/ β -gal-lipofectin complex which was prepared as follows. 3 μ g plasmid DNA and 20 μ L lipofectin reagent (GIBCO) were each diluted into 0.5mL Opti-MEM media and then mixed together. This mixture was incubated at room temperature for 15-20 min., and then the mixture (1mL) added to each 6cm plate. Transfected plates were incubated at 37°C for 5-24h, after which the plates were washed and incubated with DMEM media (GIBCO) and the cells split equally into a 96-well culture plate.

To assay melanocortin receptor analogue binding, human 293 cells expressing each of the melanocortin receptors MC-1, MC-3, MC-4 and MC-5, and mouse Y1 cells expressing the MC-2 receptor, were transiently transfected with pCRE/ β -gal as described above and assayed as follows. Two days after transfection, cells were stimulated with hormones specific for each receptor or hormone analogue by incubation for 6h at 37°C with a mixture comprising 10^{-12} - 10^{-6} M hormone or analogue, 0.1mg/mL bovine serum albumin and 0.1mM isobutylmethylxanthine in DMEM. The effect of hormone or analogue binding was determined by β -galactosidase assay according to the method of Felgner *et al.* (1994, *J. Biol. Chem.* 269: 2550-2561). Briefly, media was aspirated from

culture wells and 50 μ L lysis buffer (0.25M Tris-HCl, pH 8/0.1% Triton-X100) added to each well. Cell lysis was enhanced by one round of freezing and thawing the cell/lysis buffer mixture. 10 μ L aliquots were sampled from each well for protein determination using a commercially-available assay (BioRad, Hercules, CA). The remaining 40 μ L from each well was diluted with 40 μ L phosphate buffered saline/0.5% BSA and 150 μ L substrate buffer (60mM sodium phosphate/ 1mM MgCl₂/ 10mM KCl/ 5mM β -mercaptoethanol/ 2mg/mL *o*-nitrophenyl- β -D-galactopyranoside) added. Plates were incubated at 37°C for 1h and then absorbance at 405nm determined using a 96-well plate reader (Molecular Devices, Sunnyvale, CA). A series of two-fold dilutions from 20ng of purified β -galactosidase protein (Sigma Chemical Co, St. Louis, MO) were assayed in parallel in each experiment to enable conversion of OD₄₀₅ to known quantity of β -galactosidase protein.

The results of these experiments are shown in Figure 15. This Figure shows the results of the β -galactosidase assay described above using cells expressing each of the MC-1, MC-3, MC-4 or MC-5 receptors and contacted with α MSH or a variety of α MSH analogues, including SHU9119. These results showed that SHU9119 had relatively weak agonist activity for both the human MC-3 and MC-4 receptors.

These results demonstrated the development of a colorimetric assay for cAMP accumulation as the result of melanocortin receptor binding to agonists and antagonists.

The action of MTII, SHU9119, and the endogenous mouse *agouti* peptide as agonists or antagonists of rodent MC receptors was first determined by examining their ability to elevate intracellular cAMP in 293 cell lines expressing the rat MC3-R or mouse MC4-R (expressed as IC₅₀ values representing ligand concentration required for half-maximal inhibition of binding of (I-125)-(Nle⁴, D-Phe⁷) α -MSH tracer). Agonist/antagonist activity was also shown by demonstrating inhibition of cAMP elevation by the potent α -MSH analogue [Nle⁴, D-Phe⁷] α -MSH, using either a cAMP-responsive β -galactosidase reporter construct as described above, or by direct adenylyl cyclase assay as described in Example 3 (wherein EC₅₀ values represent ligand concentration required for half-maximal activation of a cAMP-responsive β -galactosidase reporter). Competition binding experiments were determined as the amount of radioactivity bound in the presence of 5x10⁻⁶M unlabeled [Nle⁴, D-Phe⁷] α -MSH, and was typically 3-5% of total counts bound.

In these experiments, murine *agouti* peptide was produced using a baculovirus system as described by Lu *et al.* (1994, *Nature* 371: 799-802), with the modification that the *agouti* peptide was purified from baculovirus supernatants by 0.6M NaCl step elution from an EconoS cation exchange column (BioRad). *Agouti* peptide used in these assays was approximately 60% pure.

Competition binding assays were performed to determine whether SHU9119 had antagonist activity towards α MSH binding to either the MC-3 or MC-4 receptors. These assays were performed as follows. Human 293 cells (100,000 cells/well in 24-well plates) expressing either the MC-3 or MC-4 receptors prepared as described above were incubated with a solution of 1mg/mL BSA in PBS containing 100,000cpm (3.1×10^{-10} M [125 I](Nle⁴, D-Phe⁷) α MSH and varying concentrations of α MSH, (Nle⁴, D-Phe⁷) α MSH or SHU9119. Cells were incubated for 30min at 37°C, washed twice with PBS-BSA, lysed with 0.5mL 0.5N NaOH, and counted using a γ -counter to quantitate the amount of bound [125 I](Nle⁴, D-Phe⁷) α MSH. Control experiments showed non-specific binding to occur at about 3-5% levels, and this was taken into account when analyzing the experimental results.

The SHU9119 analogue was found to be a potent antagonist of both the human MC-3 and MC-4 receptors, as shown in Figure 16. These assays showed pA₂ values of 8.3 and 9.3 for the human MC-3 and MC-4 receptors, respectively, as determined using the method of Schild (1947, *Brit. J. Pharmacol.* 2: 189-206). In contrast, no significant alteration in IC₅₀ values was detected in binding experiments using this analogue with either the MC-3 or MC-4 receptors (Figure 17).

The activity of the MTII analogue was also assayed for melanocortin receptor agonist activity. These results are shown in Figures 18A and 18B, and confirmed that the MTII analogue is a specific agonist of the MC-3 and MC-4 receptors.

Specific competition of [Nle⁴,D-Phe⁷] α -MSH binding to rat MC-3 receptor by *agouti* peptide was observed, although accurate IC₅₀ values could not be determined because the peptide preparation was not homogenous (results not shown). Specific competition of α -MSH activation of human MC4-R by *agouti* was previously disclosed (Lu *et al.*, 1994, *Nature* 371: 799-802).

EXAMPLE 5

Feeding Behavior Effect of Melanocortin Analogue Binding in Brain

The results shown in Example 4 above suggested a role in the regulation of feeding behavior in mammalian brain for MC receptor agonists and antagonists, in view of the antagonist properties of the *agouti* peptide at the MC-3 and MC-4 receptors. The *agouti* peptide was known to cause obesity when expressed ectopically in the mouse, and has been found to be a high affinity antagonist of the melanocyte stimulating hormone receptor (MC1-R) and of the hypothalamic MC-4 receptor (see Lu *et al.*, *ibid.*). The former activity explained the inhibitory effect of the *agouti* peptide on eumelanin pigment synthesis. Similarly, it was hypothesized by the inventors that *agouti* causes obesity in mice by antagonizing hypothalamic MC-4 receptors. The cyclic melanocortin analogue, SHU9119, having been shown herein and elsewhere (Hruby *et al.*) to be a specific, high affinity antagonist of the central MC-3 and MC-4 receptors, was tested for the effect of direct administration to mouse brain on feeding behavior in the animals. Intracerebroventricular (ICV) administration of SHU9119 was performed to avoid any complications caused by inhibition of peptide traverse of the blood-brain barrier.

Briefly, male C57B1/6J mice (18-29g) were maintained on a normal 12hr/12hr light dark cycle with food (Purina mouse chow) and water *ad libitum*. Animals were housed individually for 24 hrs, distributed into experimental and control groups, avoiding any bias as a function of prior weight, then injected with vehicle or vehicle plus drug just prior to the onset of a 12hr light or dark cycle. Fasted animals were deprived of food from 18:00 to 10:30 hrs to stimulate feeding during the daytime experimental period. Animals were lightly anesthetized with halothane, and administered into one lateral ventricle 2 μ L of a solution of artificial cerebrospinal fluid alone (acsf, comprising 130mM NaCl, 27mM NaHCO₃, 1.2mM Na₂HPQ, 0.3mM NaH₂PO₄, 0.5mM Na₂SO₄, 1.0mM CaCl₂, 1.0mM MgCl₂, and 2.5mM KCl), or 6nmol SHU9119 in acsf. Freehand injections were performed as described by Laursen and Belknap (1986, *J. Pharmacol. Methods* 16: 355-357) with some modifications. A 10 μ l luertip syringe (Hamilton 701LT) was fitted with a 0.5 inch 27 gauge needle. Stiff tygon tubing was slipped over the needle to expose 3mm of the needle tip. The syringe was held at a 45° angle from the front of the skull with the bevel facing up. The coronal suture was found by lightly rubbing the needle over the skull. Maintaining the 45° angle, the needle

was then inserted 1-2mm lateral to the midline, using only mild pressure to insert and remove the needle. The compounds indicated in a 2µl volume of acsf were administered slowly over approximately 15 seconds, and the needle removed after 35 seconds. Animals were allowed to recover from anesthesia and placed into a cage containing a premeasured quantity of food pellets in a spill-free cup. Moribund animals were not included in the study.

Stimulation of feeding by intracerebroventricular administration of the melanocortin antagonist SHU9119 is shown in Figures 19A through 19C. Curves show cumulative food intake as a function of time following administration of the substances shown. Figure 19A shows stimulation of feeding by administration of SHU9119 just prior to lights off (19:00 hrs) to C57B1/6J mice fed *ad libitum*. Figure 19B, in contrast, shows no effect of morning (10:00 hrs) SHU9119 administration in C57B1/6J mice fed *ad libitum*. Figure 19C illustrates stimulation of daytime feeding by SHU9119 administration in fasted C57B1/6J mice. In deriving the data points comprising these Figures, food remaining was briefly removed and weighted at the time intervals indicated. Data points indicate the mean and bars indicate standard error. Significance of the effect over time was determined by ANOVA with repeated measures. Significance of drug effects at individual time points was determined by two-way ANOVA, and is indicated in each Figure (***=P<0.001, **=P<0.01, *=P<0.05).

These results demonstrated that ICV administration of SHU9119 into one lateral ventricle of the C57B1/6J mouse just prior to lights out led to a mean 60% increase in food intake over 12 hrs (Figure 19A; P<0.005). In contrast, daytime food intake in animals fed *ad libitum* was not stimulated by administration of SHU9119 (Figure 19B). SHU9119-treatment did, however, significantly stimulate daytime food intake in animals fasted for 16 hrs prior to the experiment (Figure 19C; P<0.001). Stimulation of feeding was evident at approximately two hrs post-treatment, and continued for 12 hrs, to produce a mean 34% in food intake relative to vehicle-injected controls.

These results supported the hypothesis that *agouti* and/or SHU9119 stimulate feeding by antagonizing MC receptors in the central nervous system. To further test this hypothesis, a series of experiments were performed wherein MC receptor agonists were administered to animals primed by fasting to eat, to determine whether feeding in such animals could be inhibited by the MC receptor agonists. Animals were induced to feed

by food deprivation for 16h prior to ICV administration of the non-specific melanocortin agonist MTII. In these experiments, ICV injections in male C57B1/6J mice (20-30g) and the measurement of food intake were performed as described above.

5 Results of these experiments are shown in Figures 20A through 20C. In comparison to vehicle-injected animals, MTII was found to produce a potent inhibition of feeding within one hour after administration (Figure 20A) in a dose-responsive manner. Food intake was significantly inhibited for up to four hours following administration ($P<0.001$) at the highest dose administered (3nmol), and decreased food intake continued for the next four hours with normal rates of food intake resuming at 10 about 8 hours after treatment. This dose-responsive inhibition of feeding had an IC_{50} at the two hour time point of approximately 0.5nmol (Figure 20B). However, inhibition of feeding with 3nmol MTII was completely blocked by co-administration of 6nmol SHU9119 (Figure 20C; $P<0.001$), demonstrating that the effect results specifically from

15 Locomotor assays were performed to determine whether the effects on feeding behavior observed in these mice were secondary to generalized behavioral effects caused by administration of these melanocortin analogues. The effects of MTII on locomotor activity were tested by placing vehicle or MTII-treated mice in sound and light-proof cages containing multiple light beam detectors. These assays were performed by first 20 injecting 3nmol MTII or acsf as described above. At three hours (2:45-3:25) post-injection, 12 mice were placed into 12 separate boxes containing multiple infrared light sources and photodetectors. The boxes were contained within separate ventilated light and sound attenuating chambers (Coulbourn model E10-20). Disruption of the infrared beams, with a 10msec resolution, was tallied independently for each one minute time 25 period in each cage. The results of these assays are shown in Figure 20D. Data points indicate the mean total activity (# of light breaks) for 6 animals in each experimental group. Four way ANOVA statistical analysis was used to analyze the data, and indicated an absence of a significant difference among the two groups.

30 Inhibition of feeding by MTII could not be explained by any apparent behavioral abnormalities, or any effect on arousal or locomotor activity. MTII-treated animals appeared alert and exhibited no unusual behavior relative to controls. At approximately three hours after ICV administration, MTII-treated animals exhibited locomotor activity

that was indistinguishable from vehicle-treated animals (Figure 20D). The higher initial activity, indicative of exploratory behavior, and continued locomotion over a 15 min period was indistinguishable between the two groups, indicating that the inhibition of feeding was not due to decreased locomotion or decreased arousal.

5 The administration of MTII also inhibited food intake in three other models of hyperphagia: the C57B1/6J-*Lep^{ob}* mouse, a neuropeptide Y (NPY)-injected C57B1/6J mouse and a C57B1/6J-*A^y* mouse. Figure 21A shows inhibition of feeding by intracerebroventricular administration of MTII in *A^y* mice (females, 19-28gms). Figure 21B shows inhibition of feeding by intracerebroventricular administration of MTII in
10 C57B1/6J mice (females, 21-25gm) stimulated to feed by co-administration of NPY. Figure 21C shows inhibition of feeding by intracerebroventricular administration of the MTII in *ob/ob* mice (females, 48-69 gms). Figure 21D shows inhibition of feeding in *ob/ob* mice by intraperitoneal administration of MTII (females, 40-45 gms). ICV injections and measurement of food intake were performed as described above, with the
15 exception of NPY treated animals, which were not fasted prior to experimentation. Animals treated intraperitoneally received 100µl of a 1mM solution of MTII in saline, and vehicle injections consisted of the same amount of saline alone. Significance indicated for individual time points, determined as described above, was for 3nmol MTII vs. acsf (Figure 21A), 1.18 nmol NPY vs. 1.18 nmol NPY + 3 nmol MTII (Figure 21B),
20 3nmol MTII vs. acsf (Figure 21C), and 100 nmol MTII vs. saline (Figure 21D).

The hyperphagia in these models can be clearly seen by comparing the 12 hr food intake following a fast in vehicle-injected C57B1/6J (2.4g, Figure 19A), C57B1/6J-*A^y* (3.7g, Figure 21A) and C57B1/6J-*Lep^{ob}* (3.7g, Figure 21C) animals. As expected, MTII treatment inhibited food intake following a 16 hr fast in the C57B1/6J-*A^y* mouse (Figure
25 21A; $P < 0.05$). Interestingly, while food intake for the first four hours is significantly inhibited relative to vehicle-injected animals, it is also significantly less inhibited in the C57B1/6J-*A^y* animal than in the C57B1/6J animal given the same 3nmol dose (*compare*, Figure 20A *versus* Figure 21A, 1-4 hrs; $P < 0.001$). The decreased effectiveness of the agonist in the presence of the *A^y* allele is consistent with the proposal that this allele
30 results in chronic expression of *agouti* peptide melanocortin antagonist in the brain.

MTII, upon co-administration, also significantly inhibited the profound stimulation of feeding induced by NPY, measured over a three hr period (Figure 21C;

P<0.005). Co-administration of an approximately two-fold molar excess of MTII produced a 74% inhibition of NPY-stimulated food intake at the three hour time point.

Finally, MTII also inhibited hyperphagia due to absence of leptin in the C57B1/6J-*Lep^{ob}* mouse (Figure 21C; P<0.001). MTII potently blocked feeding (Figure 20A) in these animals, in contrast to the less potent inhibition described above for the C57B1/6J-*A^y* mouse.

The C57B1/6J-*Lep^{ob}* animal was also used to test the ability of MTII to regulate feeding when administered peripherally. Moderate doses (100nmol) of MTII inhibited feeding in the C57B1/6J-*Lep^{ob}* mouse (P<0.001) while low doses (10nmol) did not (date not shown). The kinetics were similar to those seen with ICV administration, with a potent inhibition of feeding for the first four hours. The 100-fold higher dose required peripherally, as well as the similar kinetics, suggest a primarily central nervous system-based mechanism of action of MTII.

These data show that melanocortinergergic neurons exert a tonic inhibition of feeding behavior, and that disruption of this signal leads to hyperphagia. With regard to the recently-discovered leptin hormone made by adipocytes, which is generally expressed at elevated levels in obese humans and rodents (such as the C57B1/6J-*Lep^{ob}* animal), the regulatory defect is understood to be an incapacity to respond properly to the leptin hormone signal. The instant results indicate that the melanocortins act independently, and physiologically "downstream," from the leptin hormone/receptor interaction, because it has been shown herein that melanocortin receptor agonists can potently inhibit feeding in the C57B1/6J-*Lep^{ob}* animal.

These results suggest that MC receptor agonists and antagonists can affect mammalian feeding behavior, and provide a means for determining candidate compounds for the development of effective pharmacological products directed towards alleviating such human ailments as obesity, anorexia and cachexia.

EXAMPLE 6

Use of MC Receptor-Expressing Recombinant Cells for Screening Compounds that Affect Feeding Behavior in Mammals

The results obtained in Example 5 indicated that cells expressing a variety of mammalian melanocortin receptors are useful for characterizing compounds as a first

step towards developing MC receptor agonists and antagonists for controlling feeding behavior in mammals, particularly obesity and overweight disorders in general, as well as anorexia, cachexia and other failure-to-thrive disorders.

5 A panel of mammalian melanocortin receptor-expressing recombinant cells are provided as described above in Example 3, wherein each member of the panel comprises appropriate mammalian cells, such as human 293 cells, comprising a recombinant expression construct encoding the MC-1, MC-2 (ACTH), MC-3, MC-4 or MC-5 receptor, the panel constructed to comprise cells functionally expressing each of these MC receptor proteins.

10 The panel is used as follows. Receptor agonist activity is assayed by transient or stable expression of a protein which produces a metabolite reporter molecule in response to receptor binding by any of the MC receptor proteins. An example of such a reporter system is the recombinant expression construct described in Example 4, wherein cAMP responsive elements (CREs) are operatively linked to a bacterially-
15 derived β -galactosidase (β -gal) gene. In the event of receptor binding, cAMP is produced in the mammalian cell, and the CRE induces β -gal expression. When co-incubated with a colorless substrate for β -gal, receptor binding results in conversion of the colorless substrate to a blue-colored product, which can be easily scored visually or spectrophotometrically. Alternative reporter genes, such a luciferase, can also be used
20 as reporter systems, provided that expression of the reporter molecule-producing protein is functionally linked to receptor binding of a test compound. Alternatively, cAMP production resulting from MC receptor binding can also be measured directly.

25 Assay panels are arranged so that agonist activity can be identified, quantitated and correlated with expression of each MC receptor. Automated assays using such panels are also envisioned, whereby the qualitative and quantitative detection of a reporter metabolite is detected in an array (such as a 96-well tissue culture plate) and the data collected and assembled into a computer data-base or other analytical program.

30 Antagonist activity is detected by a modification of the above assay. In this assay, the inhibition of cAMP production by a standardized amount of a known receptor agonist, specific for each receptor, is assayed in the presence of a putative antagonist compound. Production of metabolite reporter molecules and their qualitative and quantitative detection is achieved as described above, and the specificity and potency of

each antagonist compound characterized with regard to the degree of inhibition achieved for each receptor.

In view of the instant disclosure, MC-3/MC-4 receptor antagonists are expected to be useful to inhibit food intake in a hungry animal, and MC-3/MC-4 receptor agonists are expected to be useful to increase food intake in an animal. Alternative patterns of feeding behavior associated with different patterns of MC receptor agonist/antagonist activity can be determined using this assay.

Compounds having agonist or antagonist activity with the MC-3 or MC-4 receptors detected using this assay are further screened *in vivo* to determine whether the observed receptor binding activity results in modification of feeding behavior when administered to an animal. In these assays, the MC receptor binding compounds detected using the assay are administered intracranioventricularly as described above in Example 5 to animals after an overnight fast, to waking animals, or to animals that are not otherwise primed to be hungry. Feeding and locomotor activity is monitored in these animals, and compounds affecting eating behavior (either by inhibiting feeding in otherwise hungry animals or stimulating feeding in otherwise sated animals) are selected for further development.

In addition, systemic administration of compounds found to be active by ICV administration assays is used to screen such compounds for the ability to cross the blood-brain barrier. Such compounds are also useful as templates for modifications aimed at increasing the availability of these compounds in the brain after systemic administration, for increasing bioactivity, or both.

It should be understood that the foregoing disclosure emphasizes certain specific embodiments of the invention and that all modifications or alternatives equivalent thereto are within the spirit and scope of the invention as set forth in the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

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- (H) TELEFAX: 503-494-4729

- (ii) TITLE OF INVENTION: Methods and Reagents for Discovering and Using Mammalian Melanocortin Receptor Agonists and Antagonists To Modulate Feeding Behavior in Animals

- (iii) NUMBER OF SEQUENCES: 19

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: mics_feature
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: /function = "Degenerate oligonucleotide primer (sense)"
/note= "The residue at positions 24 and 24 are inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: mics_feature
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /function = "Degenerate
oligonucleotide primer (antisense)"
/note= "The residue at position 18 is inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGAATTCAG WAGGGCANCC AGCAGASRYG AA

32

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..14

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 15..959

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 960..1260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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	1				5					10							
TCT CTC AAC TCC AAT GCC ACC TCT CAC CTT GGA CTG GCC ACC AAC CAG																	98
Ser Leu Asn Ser Asn Ala Thr Ser His Leu Gly Leu Ala Thr Asn Gln																	
	15					20				25							
TCA GAG CCT TGG TGC CTG TAT GTG TCC ATC CCA GAT GGC CTC TTC CTC																	146
Ser Glu Pro Trp Cys Leu Tyr Val Ser Ile Pro Asp Gly Leu Phe Leu																	
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AGC CTA GGG CTG GTG AGT CTG GTG GAG AAT GTG CTG GTT GTG ATA GCC																	194
Ser Leu Gly Leu Val Ser Leu Val Glu Asn Val Leu Val Val Ile Ala																	
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Cys Leu Ala Leu Ser Asp Leu Met Val Ser Val Ser Ile Val Leu Glu																	
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				160					165							170	
TCC AGC ACC CTC TTT ATC ACC TAC TAC AAG CAC ACA GCC GTT CTG CTC																	578
Ser Ser Thr Leu Phe Ile Thr Tyr Tyr Lys His Thr Ala Val Leu Leu																	
				175					180							185	

TGC CTC GTC ACT TTC TTT CTA GCC ATG CTG GCA CTC ATG GCG ATT CTG Cys Leu Val Thr Phe Phe Leu Ala Met Leu Ala Leu Met Ala Ile Leu 190 195 200	626
TAT GCC CAC ATG TTC ACG AGA GCG TGC CAG CAC GTC CAG GGC ATT GCC Tyr Ala His Met Phe Thr Arg Ala Cys Gln His Val Gln Gly Ile Ala 205 210 215 220	674
CAG CTC CAC AAA AGG CGG CGG TCC ATC CGC CAA GGC TTC TGC CTC AAG Gln Leu His Lys Arg Arg Arg Ser Ile Arg Gln Gly Phe Cys Leu Lys 225 230 235	722
GGT GCT GCC ACC CTT ACT ATC CTT CTG GGG ATT TTC TTC CTG TGC TGG Gly Ala Ala Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp 240 245 250	770
GGC CCC TTC TTC CTG CAT CTC TTG CTC ATC GTC CTC TGC CCT CAG CAC Gly Pro Phe Phe Leu His Leu Leu Leu Ile Val Leu Cys Pro Gln His 255 260 265	818
CCC ACC TGC AGC TGC ATC TTC AAG AAC TTC AAC CTC TTC CTC CTC CTC Pro Thr Cys Ser Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Leu Leu 270 275 280	866
ATC GTC CTC AGC TCC ACT GTT GAC CCC CTC ATC TAT GCT TTC CGC AGC Ile Val Leu Ser Ser Thr Val Asp Pro Leu Ile Tyr Ala Phe Arg Ser 285 290 295 300	914
CAG GAG CTC CGC ATG ACA CTC AAG GAG GTG CTG CTG TGC TCC TGG Gln Glu Leu Arg Met Thr Leu Lys Glu Val Leu Leu Cys Ser Trp 305 310 315	959
TGATCAGAGG GCGCTGGGCA GAGGGTGACA GTGATATCCA GTGGCCTGCA TCTGTGAGAC	1019
CACAGGTACT CATCCCTTCC TGATCTCCAT TTGTCTAAGG GTCGACAGGA TGAGCTTTAA	1079
AATAGAAACC CAGAGTGCCT GGGGCCAGGA GAAAGGGTAA CTGTGACTGC AGGGCTCACC	1139
CAGGGCAGCT ACGGGAAGTG GAGGAGACAG GGATGGGAAC TCTAGCCCTG AGCAAGGGTC	1199
AGACCACAGG CTCCTGAAGA GCTTCACCTC TCCCCACCTA CAGGCAACTC CTGCTCAAGC	1259
C	1260

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Ser Thr Gln Glu Pro Gln Lys Ser Leu Leu Gly Ser Leu Asn Ser
 1             5             10             15

Asn Ala Thr Ser His Leu Gly Leu Ala Thr Asn Gln Ser Glu Pro Trp
      20             25             30

Cys Leu Tyr Val Ser Ile Pro Asp Gly Leu Phe Leu Ser Leu Gly Leu
      35             40             45

Val Ser Leu Val Glu Asn Val Leu Val Val Ile Ala Ile Thr Lys Asn
      50             55             60

Arg Asn Leu His Ser Pro Met Tyr Tyr Phe Ile Cys Cys Leu Ala Leu
      65             70             75             80

Ser Asp Leu Met Val Ser Val Ser Ile Val Leu Glu Thr Thr Ile Ile
      85             90             95

Leu Leu Leu Glu Val Gly Ile Leu Val Ala Arg Val Ala Leu Val Gln
      100            105            110

Gln Leu Asp Asn Leu Ile Asp Val Leu Ile Cys Gly Ser Met Val Ser
      115            120            125

Ser Leu Cys Phe Leu Gly Ile Ile Ala Ile Asp Arg Tyr Ile Ser Ile
      130            135            140

Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Arg
      145            150            155            160

Arg Ala Val Val Gly Ile Trp Met Val Ser Ile Val Ser Ser Thr Leu
      165            170            175

Phe Ile Thr Tyr Tyr Lys His Thr Ala Val Leu Leu Cys Leu Val Thr
      180            185            190

Phe Phe Leu Ala Met Leu Ala Leu Met Ala Ile Leu Tyr Ala His Met
      195            200            205

Phe Thr Arg Ala Cys Gln His Val Gln Gly Ile Ala Gln Leu His Lys
      210            215            220

Arg Arg Arg Ser Ile Arg Gln Gly Phe Cys Leu Lys Gly Ala Ala Thr
      225            230            235            240

Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro Phe Phe
      245            250            255

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Leu His Leu Leu Leu Ile Val Leu Cys Pro Gln His Pro Thr Cys Ser
 260 265 270
 Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Leu Leu Ile Val Leu Ser
 275 280 285
 Ser Thr Val Asp Pro Leu Ile Tyr Ala Phe Arg Ser Gln Glu Leu Arg
 290 295 300
 Met Thr Leu Lys Glu Val Leu Leu Cys Ser Trp
 305 310 315

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..461

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 462..1415

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 1416..1633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCGCATGTG GCCGCCCTCA ATGGAGGGCT CTGAGAACGA CTTTTAAAC GCAGAGAAAA	60
AGCTCCATTC TTCCAGACC TCAGCGCAGC CCTGCCCCAG GAAGGGAGGA GACAGAGGCC	120
AGGACGGTCC AGAGGTGTCG AAATGTCCTG GGAACCTGAG CAGCAGCCAC CAGGGAAGAG	180
GCAGGGAGGG AGCTGAGGAC CAGGCTTGGT TGTGAGAATC CCTGAGCCCA GGCGGTTGAT	240
GCCAGGAGGT GTCTGGACTG GCTGGGCCAT GCCTGGGCTG ACCTGTCCAG CCAGGGAGAG	300

GGTGTGAGGG CAGATCTGGG GGTGCCCAGA TGAAGGAGG CAGGCATGGG GACACCCAAG	360
GCCCCCTGGC AGCACCATGA ACTAAGCAGG ACACCTGGAG GGAAGAAGT GTGGGGACCT	420
GGAGGCCTCC AACGACTCCT TCCTGCTTCC TGGACAGGAC T ATG GCT GTG CAG Met Ala Val Gln 1	473
GGA TCC CAG AGA AGA CTT CTG GGC TCC CTC AAC TCC ACC CCC ACA GCC Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser Thr Pro Thr Ala 5 10 15 20	521
ATC CCC CAG CTG GGG CTG GCT GCC AAC CAG ACA GGA GCC CGG TGC CTG Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly Ala Arg Cys Leu 25 30 35	569
GAG GTG TCC ATC TCT GAC GGG CTC TTC CTC AGC CTG GGG CTG GTG AGC Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu Gly Leu Val Ser 40 45 50	617
TTG GTG GAG AAC GCG CTG GTG GTG GCC ACC ATC GCC AAG AAC CGG AAC Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala Lys Asn Arg Asn 55 60 65	665
CTG CAC TCA CCC ATG TAC TGC TTC ATC TGC TGC CTG GCC TTG TCG GAC Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu Ala Leu Ser Asp 70 75 80	713
CTG CTG GTG AGC GGG ACG AAC GTG CTG GAG ACG GCC GTC ATC CTC CTG Leu Leu Val Ser Gly Thr Asn Val Leu Glu Thr Ala Val Ile Leu Leu 85 90 95 100	761
CTG GAG GCC GGT GCA CTG GTG GCC CGG GCT GCG GTG CTG CAG CAG CTG Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val Leu Gln Gln Leu 105 110 115	809
GAC AAT GTC ATT GAC GTG ATC ACC TGC AGC TCC ATG CTG TCC AGC CTC Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met Leu Ser Ser Leu 120 125 130	857
TGC TTC CTG GGC GCC ATC GCC GTG GAC CGC TAC ATC TCC ATC TTC TAC Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile Ser Ile Phe Tyr 135 140 145	905
GCA CTG CGC TAC CAC AGC ATC GTG ACC CTG CCG CGG GCG CCG CGA GCC Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Pro Arg Ala 150 155 160	953
GTT GCG GCC ATC TGG GTG GCC AGT GTC GTC TTC AGC ACG CTC TTC ATC Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser Thr Leu Phe Ile 165 170 175 180	1001

GGC TAC TAC GAC CAC GTG GCC GTC CTG CTG TGC CTC GTG GTC TTC TTC Gly Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu Val Val Phe Phe 185 190 195	1049
CTG GCT ATG CTG GTG CTC ATG GCC GTG CTG GAC GTC CAC ATG CTG GCC Leu Ala Met Leu Val Leu Met Ala Val Leu Asp Val His Met Leu Ala 200 205 210	1097
CGG GCC TGC CAG CAC GCC CAG GGC ATC GCC CGG CTC CAC AAG AGG CAG Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu His Lys Arg Gln 215 220 225	1145
CGC CCG GTC CAC CAG GGC TTT GGC CTT AAA GGC GCT GTC ACC CTC ACC Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala Val Thr Leu Thr 230 235 240	1193
ATC CTG CTG GGC ATT TTC TTC CTC TGC TGG GGC CCC TTC TTC CTG CAT Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro Phe Phe Leu His 245 250 255 260	1241
CTC ACA CTC ATC GTC CTC TGC CCC GAG CAC CCC ACG TGC GGC TGC ATC Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr Cys Gly Cys Ile 265 270 275	1289
TTC AAG AAC TTC AAC CTC TTT CTC GCC CTC ATC ATC TGC AAT GCC ATC Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile Cys Asn Ala Ile 280 285 290	1337
ATC GAC CCC CTC ATC TAC GCC TTC CAC AGC CAG GAG CTC CGC AGG ACG Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu Leu Arg Arg Thr 295 300 305	1385
CTC AAG GAG GTG CTG ACA TGC TCC TGG TGA GCGCGGTGCA CGCGCTTTAA Leu Lys Glu Val Leu Thr Cys Ser Trp * 310 315	1435
GTGTGCTGGG CAGAGGGAGG TGGTGATATT GTGGTCTGGT TCCTGTGTGA CCCTGGGCAG	1495
TTCCTTACCT CCCTGGTCCC CGTTTGTCAA AGAGGATGGA CTAAATGATC TCTGAAAGTG	1555
TTGAAGCGCG GACCCTTCTG GGCAGGGAGG GGTCTGTCAA AACTCCAGGC AGGACTTCTC	1615
ACCAGCAGTC GTGGGAAC	1633

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
 1             5             10             15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
 20             25             30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
 35             40             45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
 50             55             60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
 65             70             75             80

Ala Leu Ser Asp Leu Leu Val Ser Gly Thr Asn Val Leu Glu Thr Ala
 85             90             95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
100             105             110

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
115             120             125

Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
130             135             140

Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
145             150             155             160

Ala Pro Arg Ala Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
165             170             175

Thr Leu Phe Ile Gly Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
180             185             190

Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Asp Val
195             200             205

His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
210             215             220

His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
225             230             235             240

Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
245             250             255

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Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
 260 265 270
 Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
 275 280 285
 Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
 290 295 300
 Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp *
 305 310 315

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2012 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..693

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 694..1587

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 1588..2012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACAACACTTT ATATATATTT TTATAAATGT AAGGGGTACA AAGGTGCCAT TTTGTTACAT	60
GGATATACCG TGTAGTGGTG AAGCCTGGGC TTTAGTGTA TCTGTCATCA GAATAACATA	120
CGTGTTACCC ATAGGAATTT CTCATCACCC GCCCCCTCCA CCCTTCGAGT CTCCAATGTC	180
CATTCCACAC TCTATATCCA CGTGTATGCA TATAGCTCCA CATATAAGTG AGAACATGTA	240
GTATTTGACT TCCTCTTTCT GAGTTATTTT ACTTTGATAA TGGCCTCCAC TTCCATCCAT	300
GTTGCTGCAA AAGACATGAC CTTATTCTTT TTGATAGCTG GGGAGTACTC CATTGTGTAT	360
ATGTACCACA TTTCTTTATC CATTACCCCA TTGAGAACAC TTAGTTGATT CCATATCTTT	420

GCTATTGTCA CTAGTGCTGC AATAAACATA CATGTGCAGG CTCCTTCTAA TATACTGATT	480
TATATTTTAT GGAGAGAGAT AGAGTTCTTA GCGAGTGTGC TGTTTATTTT TAGTGACTTT	540
GCAACTAATA TTETGTATAC TCCCTTTAGG TGATTGGAGA TTAACTTAG ATCTCCAGCA	600
AGTGCTACAA GAAGAAAAGA TCCTGAAGAA TCAATCAAGT TTCCGTGAAG TCAAGTCCAA	660
GTAACATCCC CGCCTTAACC ACAAGCAGGA GAA ATG AAG CAC ATT ATC AAC TCG	714
Met Lys His Ile Ile Asn Ser	
1 5	
TAT GAA AAC ATC AAC AAC ACA GCA AGA AAT AAT TCC GAC TGT CCT CGT	762
Tyr Glu Asn Ile Asn Asn Thr Ala Arg Asn Asn Ser Asp Cys Pro Arg	
10 15 20	
TGT GTT TTG CCG GAG GAG ATA TTT TTC ACA ATT TCC ATT GTT GGA GTT	810
Cys Val Leu Pro Glu Glu Ile Phe Phe Thr Ile Ser Ile Val Gly Val	
25 30 35	
TTG GAG AAT CTG ATC GTC CTG CTG GCT GTG TTC AAG AAT AAG AAT CTC	858
Leu Glu Asn Leu Ile Val Leu Leu Ala Val Phe Lys Asn Lys Asn Leu	
40 45 50 55	
CAG GCA CCC ATG TAC TTT TTC ATC TGT AGC TTG GCC ATA TCT GAT ATG	906
Gln Ala Pro Met Tyr Phe Phe Ile Cys Ser Leu Ala Ile Ser Asp Met	
60 65 70	
CTG GGC AGC CTA TAT AAG ATC TTG GAA AAT ATC CTG ATC ATA TTG AGA	954
Leu Gly Ser Leu Tyr Lys Ile Leu Glu Asn Ile Leu Ile Ile Leu Arg	
75 80 85	
AAC ATG GGC ATA CTC AAG CCA CGT GGC AGT TTT GAA ACC ACA GCC CAT	1002
Asn Met Gly Ile Leu Lys Pro Arg Gly Ser Phe Glu Thr Thr Ala His	
90 95 100	
GAC ATC ATC GAC TCC CTG TTT CTG CTC TCC CGT CTT GGC TCC ATC TTC	1050
Asp Ile Ile Asp Ser Leu Phe Leu Leu Ser Arg Leu Gly Ser Ile Phe	
105 110 115	
GAC CTG CTC GTG ATT GCT GCG GAC CGC TAC ATC ACC ATC TTC CAC GCA	1098
Asp Leu Leu Val Ile Ala Ala Asp Arg Tyr Ile Thr Ile Phe His Ala	
120 125 130 135	
CTG CGG TAC CAC AGC ATC GTG ACC ATG CGC CGC ACT GTG GTG GTG CTT	1146
Leu Arg Tyr His Ser Ile Val Thr Met Arg Arg Thr Val Val Val Leu	
140 145 150	
ACG GTC ATC TGG ACG TTC TGC ACG GGG ACT GGC ATC ACC ATG GTG ATC	1194
Thr Val Ile Trp Thr Phe Cys Thr Gly Thr Gly Ile Thr Met Val Ile	
155 160 165	

TTC TCC CAT CAT GTG CCC CAC GTG ATC ACC TTC ACG TCG CTG TTC CCG Phe Ser His His Val Pro His Val Ile Thr Phe Thr Ser Leu Phe Pro 170 175 180	1242
CTG ATG CTG GTC TTC ATC CTG TGC CTC TAT GTG CAC ATG TTC CTG CTG Leu Met Leu Val Phe Ile Leu Cys Leu Tyr Val His Met Phe Leu Leu 185 190 195	1290
GCT CGA TGG CAC ACC AGG AAG ATC TCC ACC CTC CCC AGA GCC AAC ATG Ala Arg Trp His Thr Arg Lys Ile Ser Thr Leu Pro Arg Ala Asn Met 200 205 210 215	1338
AAA GGG GCC ATG ACA CTG ACC ATC CTG CTC GGG GTC TTC ATC TTC TGC Lys Gly Ala Met Thr Leu Thr Ile Leu Leu Gly Val Phe Ile Phe Cys 220 225 230	1386
TGG GCC CCC TTT GTG CTT CAT GTC CTC TTG ATG ACA TTC TGC CCA AGT Trp Ala Pro Phe Val Leu His Val Leu Leu Met Thr Phe Cys Pro Ser 235 240 245	1434
AAC CCC TAC TGC GCC TGC TAC ATG TCT CTC TTC CAG GTG AAC GGC ATG Asn Pro Tyr Cys Ala Cys Tyr Met Ser Leu Phe Gln Val Asn Gly Met 250 255 260	1482
TTG ATC ATG TGC AAT GCC GTC ATT GAC CCC TTC ATA TAT GCC TTC CGG Leu Ile Met Cys Asn Ala Val Ile Asp Pro Phe Ile Tyr Ala Phe Arg 265 270 275	1530
AGC CCA GAG CTC AGG GAC GCA TTC AAA AAG ATG ATC TTC TGC AGC AGG Ser Pro Glu Leu Arg Asp Ala Phe Lys Lys Met Ile Phe Cys Ser Arg 280 285 290 295	1578
TAC TGG TAG AATGGCTGAT CCCTGGTTTT AGAATCCATG GGAATAACGT Tyr Trp *	1627
TGCCAAGTGC CAGAATAGTG TAACATTCCA ACAAATGCCA GTGCTCCTCA CTGGCCTTCC	1687
TTCCCTAATG GATGCAAGGA TGACCCACCA GCTAGTGTTT CTGAATACTA TGGCCAGGAA	1747
CAGTCTATTG TAGGGGCAAC TCTATTTGTG ACTGGACAGA TAAAACGTGT AGTAAAAGAA	1807
GGATAGAATA CAAAGTATTA GGTACAAAAG TAATTAGGTT TGCATTACTT ATGACAAATG	1867
CATTACTTTT GCACCAATCT AGTAAAACAG CAATAAAAAT TCAAGGGCTT TGGGCTAAGG	1927
CAAAGACTTG CTTTCCTGTG GACATTAACA AGCCAGTTCT GAGGCGGCCT TTCCAGGTGG	1987
AGGCCATTGC AGCCAATTTT AGAGT	2012

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Met Lys His Ile Ile Asn Ser Tyr Glu Asn Ile Asn Asn Thr Ala Arg
 1             5             10             15
Asn Asn Ser Asp Cys Pro Arg Cys Val Leu Pro Glu Glu Ile Phe Phe
      20             25             30
Thr Ile Ser Ile Val Gly Val Leu Glu Asn Leu Ile Val Leu Leu Ala
      35             40             45
Val Phe Lys Asn Lys Asn Leu Gln Ala Pro Met Tyr Phe Phe Ile Cys
      50             55             60
Ser Leu Ala Ile Ser Asp Met Leu Gly Ser Leu Tyr Lys Ile Leu Glu
      65             70             75             80
Asn Ile Leu Ile Ile Leu Arg Asn Met Gly Ile Leu Lys Pro Arg Gly
      85             90             95
Ser Phe Glu Thr Thr Ala His Asp Ile Ile Asp Ser Leu Phe Leu Leu
      100             105             110
Ser Arg Leu Gly Ser Ile Phe Asp Leu Leu Val Ile Ala Ala Asp Arg
      115             120             125
Tyr Ile Thr Ile Phe His Ala Leu Arg Tyr His Ser Ile Val Thr Met
      130             135             140
Arg Arg Thr Val Val Val Leu Thr Val Ile Trp Thr Phe Cys Thr Gly
      145             150             155             160
Thr Gly Ile Thr Met Val Ile Phe Ser His His Val Pro His Val Ile
      165             170             175
Thr Phe Thr Ser Leu Phe Pro Leu Met Leu Val Phe Ile Leu Cys Leu
      180             185             190
Tyr Val His Met Phe Leu Leu Ala Arg Trp His Thr Arg Lys Ile Ser
      195             200             205
Thr Leu Pro Arg Ala Asn Met Lys Gly Ala Met Thr Leu Thr Ile Leu
      210             215             220

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Leu Gly Val Phe Ile Phe Cys Trp Ala Pro Phe Val Leu His Val Leu
 225 230 235 240
 Leu Met Thr Phe Cys Pro Ser Asn Pro Tyr Cys Ala Cys Tyr Met Ser
 245 250 255
 Leu Phe Gln Val Asn Gly Met Leu Ile Met Cys Asn Ala Val Ile Asp
 260 265 270
 Pro Phe Ile Tyr Ala Phe Arg Ser Pro Glu Leu Arg Asp Ala Phe Lys
 275 280 285
 Lys Met Ile Phe Cys Ser Arg Tyr Trp *
 290 295

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..132

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 133..1026

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 1027..1106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGCCAGAA AGTTCCTGCT TCAGAGCAGA AGATCTTCAG CAAGAACTAC AAAGAAGAAA 60
 AGATTCTGGA GAATCAATCA AGTTTCCTGT CAAGTTCCAG TAACGTTTCT GTCTTAACTG 120
 CACACAGGAA AG ATG AAA CAC ATT CTC AAT CTG TAT GAA AAC CTC AAC 168
 Met Lys His Ile Leu Asn Leu Tyr Glu Asn Leu Asn
 1 5 10

AGT ACA GCA AGA AAT AAC TCA GAC TGT CCT GCT GTG ATT TTG CCA GAA Ser Thr Ala Arg Asn Asn Ser Asp Cys Pro Ala Val Ile Leu Pro Glu 15 20 25	216
GAG ATA TTT TTC ACA GTA TCC ATT GTT GGG GTT TTG GAG AAC CTG ATG Glu Ile Phe Phe Thr Val Ser Ile Val Gly Val Leu Glu Asn Leu Met 30 35 40	264
GTC CTT CTG GCT GTG GCC AAG AAT AAG ATG CTT CAG TCG CCC ATG TAC Val Leu Leu Ala Val Ala Lys Asn Lys Met Leu Gln Ser Pro Met Tyr 45 50 55 60	312
TTT TTC ATC TGC AGC TTG GCT ATT TCC GAT ATG CTG GGG AGC ATG TAC Phe Phe Ile Cys Ser Leu Ala Ile Ser Asp Met Leu Gly Ser Met Tyr 65 70 75	360
AAG ATT TTG GAA AAC GTT CTG ATC ATG TTC AAA AAC ATG GGT TAC CTC Lys Ile Leu Glu Asn Val Leu Ile Met Phe Lys Asn Met Gly Tyr Leu 80 85 90	408
GAG CCT CGA GGC AGT TTT GAA AGC ACA GCA GAT GAT GTG GTG GAC TCC Glu Pro Arg Gly Ser Phe Glu Ser Thr Ala Asp Asp Val Val Asp Ser 95 100 105	456
CTG TTC ATC CTC TCC CTT CTC GGC TCC ATC TGC AGC CTG TCT GTG ATT Leu Phe Ile Leu Ser Leu Leu Gly Ser Ile Cys Ser Leu Ser Val Ile 110 115 120	504
GCC GCT GAC CGC TAC ACT ACA ATC TTC CAC GCT CTG CAG TAC CAC CGC Ala Ala Asp Arg Tyr Thr Thr Ile Phe His Ala Leu Gln Tyr His Arg 125 130 135 140	552
ATC ATG ACC CCC GCA CCG TGC CCT CGT CAT CTG ACG GTC CTC TGG CGA Ile Met Thr Pro Ala Pro Cys Pro Arg His Leu Thr Val Leu Trp Arg 145 150 155	600
GGC TGC ACA GGC AGT GGC ATT ACC ATC GTG ACC TTC TCC CAT CAC GTC Gly Cys Thr Gly Ser Gly Ile Thr Ile Val Thr Phe Ser His His Val 160 165 170	648
CCC ACA GTG ATC GCC TTC ACA GCG CTG TTC CCG CTG ATG CTG GCC TTC Pro Thr Val Ile Ala Phe Thr Ala Leu Phe Pro Leu Met Leu Ala Phe 175 180 185	696
ATC CTG TGC CTC TAC GTG CAC ATG TTC CTG CTG GCC CGC TCC CAC ACC Ile Leu Cys Leu Tyr Val His Met Phe Leu Leu Ala Arg Ser His Thr 190 195 200	744
AGG AGG ACC CCC TCC CTT CCC AAA GCC AAC ATG AGA GGG GCC GTC ACA Arg Arg Thr Pro Ser Leu Pro Lys Ala Asn Met Arg Gly Ala Val Thr 205 210 215 220	792

CTG ACT GTC CTG CTC GGG GTC TTC ATT TTC TGT TGG GCA CCC TTT GTC	840
Leu Thr Val Leu Leu Gly Val Phe Ile Phe Cys Trp Ala Pro Phe Val	
225 230 235	
CTT CAT GTC CTC TTG ATG ACA TTC TGC CCA GCT GAC CCC TAC TGT GCC	888
Leu His Val Leu Leu Met Thr Phe Cys Pro Ala Asp Pro Tyr Cys Ala	
240 245 250	
TGC TAC ATG TCC CTC TTC CAG GTG AAT GGT GTG TTG ATC ATG TGT AAT	936
Cys Tyr Met Ser Leu Phe Gln Val Asn Gly Val Leu Ile Met Cys Asn	
255 260 265	
GCC ATC ATC GAC CCC TTC ATA TAT GCC TTT CGG AGC CCA GAG CTC AGG	984
Ala Ile Ile Asp Pro Phe Ile Tyr Ala Phe Arg Ser Pro Glu Leu Arg	
270 275 280	
GTC GCA TTC AAA AAG ATG GTT ATC TGC AAC TGT TAC CAG TAG	1026
Val Ala Phe Lys Lys Met Val Ile Cys Asn Cys Tyr Gln *	
285 290 295	
AATGATTGGT CCCTGATTTT AGGAGCCACA GGGATATACT GTCAGGGACA GAGTAGCGTG	1086
ACAGACCAAC AACACTAGGA CT	1108

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Lys His Ile Leu Asn Leu Tyr Glu Asn Leu Asn Ser Thr Ala Arg	
1 5 10 15	
Asn Asn Ser Asp Cys Pro Ala Val Ile Leu Pro Glu Glu Ile Phe Phe	
20 25 30	
Thr Val Ser Ile Val Gly Val Leu Glu Asn Leu Met Val Leu Leu Ala	
35 40 45	
Val Ala Lys Asn Lys Met Leu Gln Ser Pro Met Tyr Phe Phe Ile Cys	
50 55 60	
Ser Leu Ala Ile Ser Asp Met Leu Gly Ser Met Tyr Lys Ile Leu Glu	
65 70 75 80	

Asn	Val	Leu	Ile	Met	Phe	Lys	Asn	Met	Gly	Tyr	Leu	Glu	Pro	Arg	Gly	
				85					90					95		
Ser	Phe	Glu	Ser	Thr	Ala	Asp	Asp	Val	Val	Asp	Ser	Leu	Phe	Ile	Leu	
				100					105					110		
Ser	Leu	Leu	Gly	Ser	Ile	Cys	Ser	Leu	Ser	Val	Ile	Ala	Ala	Asp	Arg	
				115					120					125		
Tyr	Thr	Thr	Ile	Phe	His	Ala	Leu	Gln	Tyr	His	Arg	Ile	Met	Thr	Pro	
				130					135					140		
Ala	Pro	Cys	Pro	Arg	His	Leu	Thr	Val	Leu	Trp	Arg	Gly	Cys	Thr	Gly	
				145					150					155		
Ser	Gly	Ile	Thr	Ile	Val	Thr	Phe	Ser	His	His	Val	Pro	Thr	Val	Ile	
				165					170					175		
Ala	Phe	Thr	Ala	Leu	Phe	Pro	Leu	Met	Leu	Ala	Phe	Ile	Leu	Cys	Leu	
				180					185					190		
Tyr	Val	His	Met	Phe	Leu	Leu	Ala	Arg	Ser	His	Thr	Arg	Arg	Thr	Pro	
				195					200					205		
Ser	Leu	Pro	Lys	Ala	Asn	Met	Arg	Gly	Ala	Val	Thr	Leu	Thr	Val	Leu	
				210					215					220		
Leu	Gly	Val	Phe	Ile	Phe	Cys	Trp	Ala	Pro	Phe	Val	Leu	His	Val	Leu	
				225					230					235		
Leu	Met	Thr	Phe	Cys	Pro	Ala	Asp	Pro	Tyr	Cys	Ala	Cys	Tyr	Met	Ser	
				245					250					255		
Leu	Phe	Gln	Val	Asn	Gly	Val	Leu	Ile	Met	Cys	Asn	Ala	Ile	Ile	Asp	
				260					265					270		
Pro	Phe	Ile	Tyr	Ala	Phe	Arg	Ser	Pro	Glu	Leu	Arg	Val	Ala	Phe	Lys	
				275					280					285		
Lys	Met	Val	Ile	Cys	Asn	Cys	Tyr	Gln	*							
				290					295							

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

(A) NAME/KEY: 5'UTR

(B) LOCATION: 1..297

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 298..1269

(ix) FEATURE:

(A) NAME/KEY: 3'UTR

(B) LOCATION: 1270..1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCTGTA	ACT	GTAGCA	ACCG	GTGTT	GGGTG	GGGAT	GAGAA	GAGAC	CAGAG	AGAGAG	AGGG	60				
TCAGAG	CGAC	AGGGG	ATGAG	ACAGG	CTGGT	CAGAG	TCTGC	ACTGA	TGTT	GGAGAC	GCAA	120				
AGGAA	AGTTT	TTTCT	ATGTC	TCCA	ACCTCC	CCCTC	CTCCC	CCGTT	TCTCT	CTGGAG	AAAC	180				
TAAA	ATGTAG	ACTGG	ACAGC	ATCCA	CAAGA	GAAGC	ACCTA	GAAGA	AGATT	TTTTTT	TCCC	240				
AGCAG	CTTGC	TCAGG	ACCCT	GCAGG	AGCTG	CAGCC	GGAAC	TGGT	CCCC	GCC	GATA	ACC	297			
ATG	AAC	TCT	TCC	TGC	TGC	CCG	TCC	TCT	TAT	CCG	ACG	CTG	CCT	AAC	345	
Met	Asn	Ser	Ser	Cys	Cys	Pro	Ser	Ser	Ser	Tyr	Pro	Thr	Leu	Pro	Asn	
1				5				10				15				
CTC	TCC	CAG	CAC	CCT	GCA	GCC	CCC	TCT	GCC	AGC	AAC	CGG	AGT	GGC	AGT	393
Leu	Ser	Gln	His	Pro	Ala	Ala	Pro	Ser	Ala	Ser	Asn	Arg	Ser	Gly	Ser	
			20					25				30				
GGG	TTC	TGC	GAG	CAG	GTT	TTC	ATC	AAG	CCA	GAG	GTC	TTC	CTG	GCA	CTG	441
Gly	Phe	Cys	Glu	Gln	Val	Phe	Ile	Lys	Pro	Glu	Val	Phe	Leu	Ala	Leu	
		35						40				45				
GGC	ATC	GTC	AGT	CTG	ATG	GAA	AAC	ATC	CTG	GTG	ATC	CTG	GCT	GTG	GTG	489
Gly	Ile	Val	Ser	Leu	Met	Glu	Asn	Ile	Leu	Val	Ile	Leu	Ala	Val	Val	
		50						55				60				
AGG	AAC	GGC	AAC	CTG	CAC	TCC	CCC	ATG	TAC	TTC	TTC	CTG	CTG	AGC	CTG	537
Arg	Asn	Gly	Asn	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Leu	Ser	Leu	
		65				70				75				80		
CTG	CAG	GCC	GAC	CTG	CTG	GTG	AGC	CTG	TCC	AAC	TCC	CTG	GAG	ACC	ATC	585
Leu	Gln	Ala	Asp	Leu	Leu	Val	Ser	Leu	Ser	Asn	Ser	Leu	Glu	Thr	Ile	
				85						90				95		

ATG ATC GTG GTT ATC AAC AGC GAC TCC CTG ACC TTG GAG GAC CAA TTC	633
Met Ile Val Val Ile Asn Ser Asp Ser Leu Thr Leu Glu Asp Gln Phe	
100 105 110	
ATC CAG CAC ATG GAC AAC ATC TTC GAC TCT ATG ATC TGC ATC TCC CTG	681
Ile Gln His Met Asp Asn Ile Phe Asp Ser Met Ile Cys Ile Ser Leu	
115 120 125	
GTG GCC TCC ATC TGC AAC CTC CTG GCC ATC GCC GTG GAC AGG TAC GTC	729
Val Ala Ser Ile Cys Asn Leu Leu Ala Ile Ala Val Asp Arg Tyr Val	
130 135 140	
ACC ATC TTC TAT GCC CTC CGT TAC CAC AGC ATC ATG ACG GTT AGG AAA	777
Thr Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Met Thr Val Arg Lys	
145 150 155 160	
GCC CTC TCC TTG ATC GTG GCC ATC TGG GTC TGC TGT GGC ATC TGC GGC	825
Ala Leu Ser Leu Ile Val Ala Ile Trp Val Cys Cys Gly Ile Cys Gly	
165 170 175	
GTG ATG TTC ATC GTC TAC TCC GAG AGC AAG ATG GTC ATC GTG TGC CTC	873
Val Met Phe Ile Val Tyr Ser Glu Ser Lys Met Val Ile Val Cys Leu	
180 185 190	
ATC ACC ATG TTC TTC GCC ATG GTG CTC CTC ATG GGC ACC CTG TAC ATC	921
Ile Thr Met Phe Phe Ala Met Val Leu Leu Met Gly Thr Leu Tyr Ile	
195 200 205	
CAC ATG TTC CTC TTC GCC AGG CTG CAC GTC CAG CGC ATC GCG GCA CTG	969
His Met Phe Leu Phe Ala Arg Leu His Val Gln Arg Ile Ala Ala Leu	
210 215 220	
CCA CCT GCT GAC GGG CTA GCC CCG CAG CAG CAC TCG TGC ATG AAG GGG	1017
Pro Pro Ala Asp Gly Leu Ala Pro Gln Gln His Ser Cys Met Lys Gly	
225 230 235 240	
GCC GTC ACC ATC ACC ATC CTG CTG GGG GTT TTC ATC TTC TGC TGG GCG	1065
Ala Val Thr Ile Thr Ile Leu Leu Gly Val Phe Ile Phe Cys Trp Ala	
245 250 255	
CCT TTC TTC CTC CAC CTG GTC CTC ATC ATC ACC TGC CCC ACC AAC CCC	1113
Pro Phe Phe Leu His Leu Val Leu Ile Ile Thr Cys Pro Thr Asn Pro	
260 265 270	
TAC TGC ATC TGC TAC ACG GCG CAC TTC AAC ACC TAC CTG GTT CTC ATC	1161
Tyr Cys Ile Cys Tyr Thr Ala His Phe Asn Thr Tyr Leu Val Leu Ile	
275 280 285	
ATG TGC AAC TCT GTC ATC GAC CCC CTC ATC TAC GCC TTC CGC AGC CTG	1209
Met Cys Asn Ser Val Ile Asp Pro Leu Ile Tyr Ala Phe Arg Ser Leu	
290 295 300	

GAG CTG CGA AAC ACC TTC AAG GAG ATT CTC TGC GGT TGC AAT GGC ATG 1257
 Glu Leu Arg Asn Thr Phe Lys Glu Ile Leu Cys Gly Cys Asn Gly Met
 305 310 315 320

AAC GTG GGC TAG GAACCCCGA GGAGGTGTTT CACGGCTAGC CAAGAGAGAA 1309
 Asn Val Gly * *

AAGCAATGCT CAGGTGAGAC ACAGAAGGG 1338

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Asn	Ser	Ser	Cys	Cys	Pro	Ser	Ser	Ser	Tyr	Pro	Thr	Leu	Pro	Asn	1	5	10	15
Leu	Ser	Gln	His	Pro	Ala	Ala	Pro	Ser	Ala	Ser	Asn	Arg	Ser	Gly	Ser	20	25	30	
Gly	Phe	Cys	Glu	Gln	Val	Phe	Ile	Lys	Pro	Glu	Val	Phe	Leu	Ala	Leu	35	40	45	
Gly	Ile	Val	Ser	Leu	Met	Glu	Asn	Ile	Leu	Val	Ile	Leu	Ala	Val	Val	50	55	60	
Arg	Asn	Gly	Asn	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Leu	Ser	Leu	65	70	75	80
Leu	Gln	Ala	Asp	Leu	Leu	Val	Ser	Leu	Ser	Asn	Ser	Leu	Glu	Thr	Ile	85	90	95	
Met	Ile	Val	Val	Ile	Asn	Ser	Asp	Ser	Leu	Thr	Leu	Glu	Asp	Gln	Phe	100	105	110	
Ile	Gln	His	Met	Asp	Asn	Ile	Phe	Asp	Ser	Met	Ile	Cys	Ile	Ser	Leu	115	120	125	
Val	Ala	Ser	Ile	Cys	Asn	Leu	Leu	Ala	Ile	Ala	Val	Asp	Arg	Tyr	Val	130	135	140	
Thr	Ile	Phe	Tyr	Ala	Leu	Arg	Tyr	His	Ser	Ile	Met	Thr	Val	Arg	Lys	145	150	155	160

Ala Leu Ser Leu Ile Val Ala Ile Trp Val Cys Cys Gly Ile Cys Gly
 165 170 175

Val Met Phe Ile Val Tyr Ser Glu Ser Lys Met Val Ile Val Cys Leu
 180 185 190

Ile Thr Met Phe Phe Ala Met Val Leu Leu Met Gly Thr Leu Tyr Ile
 195 200 205

His Met Phe Leu Phe Ala Arg Leu His Val Gln Arg Ile Ala Ala Leu
 210 215 220

Pro Pro Ala Asp Gly Leu Ala Pro Gln Gln His Ser Cys Met Lys Gly
 225 230 235 240

Ala Val Thr Ile Thr Ile Leu Leu Gly Val Phe Ile Phe Cys Trp Ala
 245 250 255

Pro Phe Phe Leu His Leu Val Leu Ile Ile Thr Cys Pro Thr Asn Pro
 260 265 270

Tyr Cys Ile Cys Tyr Thr Ala His Phe Asn Thr Tyr Leu Val Leu Ile
 275 280 285

Met Cys Asn Ser Val Ile Asp Pro Leu Ile Tyr Ala Phe Arg Ser Leu
 290 295 300

Glu Leu Arg Asn Thr Phe Lys Glu Ile Leu Cys Gly Cys Asn Gly Met
 305 310 315 320

Asn Val Gly *

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: mics_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /function = "Degenerate
 oligonucleotide primer (sense)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGTCGACCR CCCATGTAYT DYTTCATCTG

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..393

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 394..1389

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 1390..1671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

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AGCTTCCGAG AGGCAGCCGA TGTGAGCATG TGCGCACAGA TTCGTCTCCC AATGGCATGG      60
CAGCTTCAAG GAAAATTATT TTGAACAGAC TTGAATGCAT AAGATTAAAG TTAAAGCAGA      120
AGTGAGAACA AGAAAGCAAA GAGCAGACTC TTTCAACTGA GAATGAATAT TTTGAAGCCC      180
AAGATTTTAA CGTGATGATG ATTAGAGTCG TACCTAAAAG AGACTAAAAA CTCCATGTCA      240
AGCTCTGGAC TTGTGACATT TACTCACAGC AGGCATGGCA ATTTTAGCCT CACAACTTTC      300
AGACAGATAA AGACTTGGAG GAAATAACTG AGACGACTCC CTGACCCAGG AGGTTAAATC      360
AATTCAGGGG GACACTGGAA TTCTCCTGCC AGC ATG GTG AAC TCC ACC CAC CGT      414
                               Met Val Asn Ser Thr His Arg
                               1               5

GGG ATG CAC ACT TCT CTG CAC CTC TGG AAC CGC AGC AGT TAC AGA CTG      462
Gly Met His Thr Ser Leu His Leu Trp Asn Arg Ser Ser Tyr Arg Leu
      10               15               20

CAC AGC AAT GCC AGT GAG TCC CTT GGA AAA GGC TAC TCT GAT GGA GGG      510
His Ser Asn Ala Ser Glu Ser Leu Gly Lys Gly Tyr Ser Asp Gly Gly
      25               30               35

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TGC	TAC	GCG	CAA	CTT	TTT	GTC	TCT	CCT	GAG	GTG	TTT	GTG	ACT	CTG	GGT	558
Cys	Tyr	Ala	Gln	Leu	Phe	Val	Ser	Pro	Glu	Val	Phe	Val	Thr	Leu	Gly	
40					45					50					55	
GTG	ATC	AGC	TTG	TTG	GAG	AAT	ATC	TTA	GAG	ATT	GTG	GCA	ATA	GCC	AAG	606
Val	Ile	Ser	Leu	Leu	Glu	Asn	Ile	Leu	Glu	Ile	Val	Ala	Ile	Ala	Lys	
				60					65					70		
AAC	AAG	AAT	CTG	CAT	TCA	CCC	ATG	TAC	TTT	TTC	ATC	TGC	AGC	TTG	GCT	654
Asn	Lys	Asn	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe	Ile	Cys	Ser	Leu	Ala	
			75					80					85			
GTG	GCT	GAT	ATG	CTG	GTG	AGC	GTT	TCA	AAT	GGA	TCA	GAA	ACC	ATT	ATC	702
Val	Ala	Asp	Met	Leu	Val	Ser	Val	Ser	Asn	Gly	Ser	Glu	Thr	Ile	Ile	
			90				95					100				
ATC	ACC	CTA	TTA	AAC	CGT	ACA	GAT	ACG	GAT	GCA	CAG	AGT	TTC	ACA	GTG	750
Ile	Thr	Leu	Leu	Asn	Arg	Thr	Asp	Thr	Asp	Ala	Gln	Ser	Phe	Thr	Val	
	105					110					115					
AAT	ATT	GAT	AAT	GTC	ATT	GAC	TCG	GTG	ATC	TGT	AGC	TCC	TTG	CTT	GCA	798
Asn	Ile	Asp	Asn	Val	Ile	Asp	Ser	Val	Ile	Cys	Ser	Ser	Leu	Leu	Ala	
120					125					130					135	
TCC	ATT	TGC	AGC	CTG	CTT	TCA	ATT	GCA	GTG	GAC	AGG	TAC	TTT	ACT	ATC	846
Ser	Ile	Cys	Ser	Leu	Leu	Ser	Ile	Ala	Val	Asp	Arg	Tyr	Phe	Thr	Ile	
				140					145					150		
TTC	TAT	GCT	CTC	CAG	TAC	CAT	AAC	ATT	ATG	ACA	GTT	AAG	CGG	GTT	GGG	894
Phe	Tyr	Ala	Leu	Gln	Tyr	His	Asn	Ile	Met	Thr	Val	Lys	Arg	Val	Gly	
			155					160					165			
ATC	AGC	ATA	AGT	TGT	ATC	TGG	GCA	GCT	TGC	ACG	GTT	TCA	GGT	ATT	TTG	942
Ile	Ser	Ile	Ser	Cys	Ile	Trp	Ala	Ala	Cys	Thr	Val	Ser	Gly	Ile	Leu	
		170					175					180				
TTC	ATC	ATT	TAC	TCA	GAT	AGT	AGT	GCT	GTC	ATC	ATC	TGC	CTC	ATC	ACC	990
Phe	Ile	Ile	Tyr	Ser	Asp	Ser	Ser	Ala	Val	Ile	Ile	Cys	Leu	Ile	Thr	
	185					190					195					
ATG	TTC	TTC	ACC	ATG	CTG	GCT	CTC	ATG	GCT	TCT	CTC	TAT	GTC	CAC	CTG	1038
Met	Phe	Phe	Thr	Met	Leu	Ala	Leu	Met	Ala	Ser	Leu	Tyr	Val	His	Leu	
200					205					210					215	
TTC	CTG	ATG	GCC	AGG	CTT	CAC	ATT	AAG	AGG	ATT	GCT	GTC	CTC	CCC	GGC	1086
Phe	Leu	Met	Ala	Arg	Leu	His	Ile	Lys	Arg	Ile	Ala	Val	Leu	Pro	Gly	
				220					225					230		
ACT	GGT	GCC	ATC	CGC	CAA	GGT	GCC	AAT	ATG	AAG	GGA	GCG	ATT	ACC	TTG	1134
Thr	Gly	Ala	Ile	Arg	Gln	Gly	Ala	Asn	Met	Lys	Gly	Ala	Ile	Thr	Leu	
			235					240						245		

ACC ATC CTG ATT GGC GTC TTT GTT GTC TGC TGG GCC CCA TTC TTC CTC	1182
Thr Ile Leu Ile Gly Val Phe Val Val Cys Trp Ala Pro Phe Phe Leu	
250 255 260	
CAC TTA ATA TTC TAC ATC TCT TGT CCT CAG AAT CCA TAT TGT GTG TGC	1230
His Leu Ile Phe Tyr Ile Ser Cys Pro Gln Asn Pro Tyr Cys Val Cys	
265 270 275	
TTC ATG TCT CAC TTT AAC TTG TAT CTC ATA CTG ATC ATG TGT AAT TCA	1278
Phe Met Ser His Phe Asn Leu Tyr Leu Ile Leu Ile Met Cys Asn Ser	
280 285 290 295	
ATC ATC GAT CCT CTG ATT TAT GCA CTC CGG AGT CAA GAA CTG AGG AAA	1326
Ile Ile Asp Pro Leu Ile Tyr Ala Leu Arg Ser Gln Glu Leu Arg Lys	
300 305 310	
ACC TTC AAA GAG ATC ATC TCT TCC TAT CCC CTG GGA GGC CTT TGT GAC	1374
Thr Phe Lys Glu Ile Ile Ser Ser Tyr Pro Leu Gly Gly Leu Cys Asp	
315 320 325	
TTG TCT AGC AGA TAT TAAATGGGGA CAGAGCACGC AATATAGGAA CATCCATAAG	1429
Leu Ser Ser Arg Tyr	
330	
AGACTTTTTC ACTCTTACCC TACCTGAATA TTCTACTTCT GCAACAGCTT TCTCTTCCGT	1489
GTAGGGTACT GGTGAGATA TCCATTGTGT AAATTTAAGC CTATGATTTT TAATGAGAAA	1549
AAATGCCAG TCTCTGTATT ATTTCCAATC TCATGCTACT TTTTGGCCA TAAATATGA	1609
ATCTATGTTA TAGGTTGTAG GCACTGTGGA TTTACAAAAA GAAAAGTCCT TATTAAAAGA	1669
TT	1671

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Val Asn Ser Thr His Arg Gly Met His Thr Ser Leu His Leu Trp
1 5 10 15
Asn Arg Ser Ser Tyr Arg Leu His Ser Asn Ala Ser Glu Ser Leu Gly
20 25 30

Lys Gly Tyr Ser Asp Gly Gly Cys Tyr Ala Gln Leu Phe Val Ser Pro
 35 40 45
 Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu
 50 55 60
 Glu Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr
 65 70 75 80
 Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser
 85 90 95
 Asn Gly Ser Glu Thr Ile Ile Ile Thr Leu Leu Asn Arg Thr Asp Thr
 100 105 110
 Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val
 115 120 125
 Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala
 130 135 140
 Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile
 145 150 155 160
 Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala
 165 170 175
 Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala
 180 185 190
 Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met
 195 200 205
 Ala Ser Leu Tyr Val His Leu Phe Leu Met Ala Arg Leu His Ile Lys
 210 215 220
 Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn
 225 230 235 240
 Met Lys Gly Ala Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val
 245 250 255
 Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro
 260 265 270
 Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu
 275 280 285
 Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu
 290 295 300

Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Ser Ser Tyr
 305 310 315 320

Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr
 325 330

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATG AAC TCC TCC TCC ACC CTG ACT GTA TTG AAT CTT ACC CTG AAC GCC	48
Met Asn Ser Ser Ser Thr Leu Thr Val Leu Asn Leu Thr Leu Asn Ala	
1 5 10 15	
TCA GAG GAT GGC ATT TTA GGA TCA AAT GTC AAG AAC AAG TCT TTG GCC	96
Ser Glu Asp Gly Ile Leu Gly Ser Asn Val Lys Asn Lys Ser Leu Ala	
20 25 30	
TGT GAA GAA ATG GGC ATT GCC GTG GAG GTG TTC CTG ACC CTG GGT CTC	144
Cys Glu Glu Met Gly Ile Ala Val Glu Val Phe Leu Thr Leu Gly Leu	
35 40 45	
GTC AGC CTC TTA GAG AAC ATC CTG GTC ATT GGG GCC ATA GTA AAG AAC	192
Val Ser Leu Leu Glu Asn Ile Leu Val Ile Gly Ala Ile Val Lys Asn	
50 55 60	
AAA AAC CTG CAC TCA CCC ATG TAC TTC TTT GTG GGC AGC TTA GCC GTG	240
Lys Asn Leu His Ser Pro Met Tyr Phe Phe Val Gly Ser Leu Ala Val	
65 70 75 80	
GCC GAC ATG CTG GTG AGC ATG TCC AAT GCC TGG GAG ACT GTC ACC ATA	288
Ala Asp Met Leu Val Ser Met Ser Asn Ala Trp Glu Thr Val Thr Ile	
85 90 95	
TAC TTG CTA AAT AAT AAA CAC CTG GTG ATA GCC GAC ACC TTT GTG CGA	336
Tyr Leu Leu Asn Asn Lys His Leu Val Ile Ala Asp Thr Phe Val Arg	
100 105 110	

CAC ATC GAC AAC GTG TTC GAC TCC ATG ATC TGC ATC TCT GTG GTG GCC	384
His Ile Asp Asn Val Phe Asp Ser Met Ile Cys Ile Ser Val Val Ala	
115 120 125	
TCG ATG TGC AGT TTG CTG GCC ATT GCG GTG GAT AGG TAC ATC ACC ATC	432
Ser Met Cys Ser Leu Leu Ala Ile Ala Val Asp Arg Tyr Ile Thr Ile	
130 135 140	
TTC TAT GCC TTG CGC TAC CAC CAC ATC ATG ACC GCG AGG CGC TCG GGG	480
Phe Tyr Ala Leu Arg Tyr His His Ile Met Thr Ala Arg Arg Ser Gly	
145 150 155 160	
GTG ATC ATC GCC TGC ATT TGG ACC TTC TGC ATA AGC TGC GGC ATT GTT	528
Val Ile Ile Ala Cys Ile Trp Thr Phe Cys Ile Ser Cys Gly Ile Val	
165 170 175	
TTC ATC ATC TAC TAT GAG TCC AAG TAT GTG ATC ATT TGC CTC ATC TCC	576
Phe Ile Ile Tyr Tyr Glu Ser Lys Tyr Val Ile Ile Cys Leu Ile Ser	
180 185 190	
ATG TTC TTC ACC ATG CTG TTC TTC ATG GTG TCT CTG TAT ATA CAC ATG	624
Met Phe Phe Thr Met Leu Phe Phe Met Val Ser Leu Tyr Ile His Met	
195 200 205	
TTC CTC CTG GCC CGG AAC CAT GTC AAG CGG ATA GCA GCT TCC CCC AGA	672
Phe Leu Leu Ala Arg Asn His Val Lys Arg Ile Ala Ala Ser Pro Arg	
210 215 220	
TAC AAC TCC GTG AGG CAA AGG ACC AGC ATG AAG GGG GCT ATT ACC CTC	720
Tyr Asn Ser Val Arg Gln Arg Thr Ser Met Lys Gly Ala Ile Thr Leu	
225 230 235 240	
ACC ATG CTA CTG GGG ATT TTC ATT GTC TGC TGG TCT CCC TTC TTT CTT	768
Thr Met Leu Leu Gly Ile Phe Ile Val Cys Trp Ser Pro Phe Phe Leu	
245 250 255	
CAC CTT ATC TTA ATG ATC TCC TGC CCT CAG AAC GTC TAC TGC TCT TGC	816
His Leu Ile Leu Met Ile Ser Cys Pro Gln Asn Val Tyr Cys Ser Cys	
260 265 270	
TTT ATG TCT TAC TTC AAC ATG TAC CTT ATA CTC ATC ATG TGC AAC TCC	864
Phe Met Ser Tyr Phe Asn Met Tyr Leu Ile Leu Ile Met Cys Asn Ser	
275 280 285	
GTG ATC GAT CCT CTC ATC TAC GCC CTC CGC AGC CAA GAG ATG CGG AGG	912
Val Ile Asp Pro Leu Ile Tyr Ala Leu Arg Ser Gln Glu Met Arg Arg	
290 295 300	
ACC TTT AAG GAG ATC GTC TGT TGT CAC GGA TTC CGG CGA CCT TGT AGG	960
Thr Phe Lys Glu Ile Val Cys Cys His Gly Phe Arg Arg Pro Cys Arg	
305 310 315 320	

CTC CTT GGC GGG TAT TAA
 Leu Leu Gly Gly Tyr
 325

978

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Asn	Ser	Ser	Ser	Thr	Leu	Thr	Val	Leu	Asn	Leu	Thr	Leu	Asn	Ala	1	5	10	15
Ser	Glu	Asp	Gly	Ile	Leu	Gly	Ser	Asn	Val	Lys	Asn	Lys	Ser	Leu	Ala	20	25	30	
Cys	Glu	Glu	Met	Gly	Ile	Ala	Val	Glu	Val	Phe	Leu	Thr	Leu	Gly	Leu	35	40	45	
Val	Ser	Leu	Leu	Glu	Asn	Ile	Leu	Val	Ile	Gly	Ala	Ile	Val	Lys	Asn	50	55	60	
Lys	Asn	Leu	His	Ser	Pro	Met	Tyr	Phe	Phe	Val	Gly	Ser	Leu	Ala	Val	65	70	75	80
Ala	Asp	Met	Leu	Val	Ser	Met	Ser	Asn	Ala	Trp	Glu	Thr	Val	Thr	Ile	85	90	95	
Tyr	Leu	Leu	Asn	Asn	Lys	His	Leu	Val	Ile	Ala	Asp	Thr	Phe	Val	Arg	100	105	110	
His	Ile	Asp	Asn	Val	Phe	Asp	Ser	Met	Ile	Cys	Ile	Ser	Val	Val	Ala	115	120	125	
Ser	Met	Cys	Ser	Leu	Leu	Ala	Ile	Ala	Val	Asp	Arg	Tyr	Ile	Thr	Ile	130	135	140	
Phe	Tyr	Ala	Leu	Arg	Tyr	His	His	Ile	Met	Thr	Ala	Arg	Arg	Ser	Gly	145	150	155	160
Val	Ile	Ile	Ala	Cys	Ile	Trp	Thr	Phe	Cys	Ile	Ser	Cys	Gly	Ile	Val	165	170	175	

Phe Ile Ile Tyr Tyr Glu Ser Lys Tyr Val Ile Ile Cys Leu Ile Ser
 180 185 190
 Met Phe Phe Thr Met Leu Phe Phe Met Val Ser Leu Tyr Ile His Met
 195 200 205
 Phe Leu Leu Ala Arg Asn His Val Lys Arg Ile Ala Ala Ser Pro Arg
 210 215 220
 Tyr Asn Ser Val Arg Gln Arg Thr Ser Met Lys Gly Ala Ile Thr Leu
 225 230 235 240
 Thr Met Leu Leu Gly Ile Phe Ile Val Cys Trp Ser Pro Phe Phe Leu
 245 250 255
 His Leu Ile Leu Met Ile Ser Cys Pro Gln Asn Val Tyr Cys Ser Cys
 260 265 270
 Phe Met Ser Tyr Phe Asn Met Tyr Leu Ile Leu Ile Met Cys Asn Ser
 275 280 285
 Val Ile Asp Pro Leu Ile Tyr Ala Leu Arg Ser Gln Glu Met Arg Arg
 290 295 300
 Thr Phe Lys Glu Ile Val Cys Cys His Gly Phe Arg Arg Pro Cys Arg
 305 310 315 320
 Leu Leu Gly Gly Tyr
 325

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /function = "Degenerate
oligonucleotide primer (antisense)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGACG TCACAGTATG ACGGCCATGG

30

WHAT WE CLAIM IS:

1. A method for characterizing a compound as an agonist of a mammalian melanocortin receptor, the method comprising the steps of:

5 (a) providing a panel comprising a first mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the α -MSH receptor, a second mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the ACTH receptor, a third mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-3 receptor, a fourth mammalian cell
10 comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-4 receptor, and a fifth mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-5 receptor, wherein each mammalian cell expresses the melanocortin receptor encoded by the recombinant expression construct comprising the cell;

15 (b) contacting each of the cells of the panel with a test compound to be characterized as an agonist of a mammalian melanocortin receptor;

(c) detecting binding of the test compound to each of the mammalian melanocortin receptors by assaying for a metabolite produced in the cells that bind the compound.

20

2. The method of claim 1, wherein the metabolite detected in subpart (c) is cyclic AMP.

25 3. The method of claim 1, each of the cells further comprising a recombinant expression construct encoding a cyclic AMP responsive element (CRE) transcription factor binding site operatively linked to a nucleic acid sequence encoding a protein capable of producing a detectable metabolite.

30 4. The method of claim 3, wherein the nucleic acid sequence encodes β -galactosidase.

5. The method of claim 3, wherein the recombinant expression construct is pCRE/ β -galactosidase.

6. The method of claim 3, wherein the detectable metabolite produced by the protein encoded by the recombinant expression construct is produced by binding of the test compound to the mammalian melanocortin receptor encoded by each of the cells of the panel.

7. A method for characterizing a compound as an antagonist of a mammalian melanocortin receptor, the method comprising the steps of:

(a) providing a panel comprising a first mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the α -MSH receptor, a second mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the ACTH receptor, a third mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-3 receptor, a fourth mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-4 receptor, and a fifth mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-5 receptor, wherein each mammalian cell expresses the melanocortin receptor encoded by the recombinant expression construct comprising the cell;

(b) contacting each of the cells of the panel with an agonist of the mammalian melanocortin receptor in an amount sufficient to produce a detectable amount of a metabolite produced in the cells that bind the agonist, in the presence or absence of a test compound to be characterized as an antagonist of a mammalian melanocortin receptor;

(c) detecting the amount of the metabolite produced in each cell in the panel in the presence of the test compound with the amount of the metabolite produced in each cell in the panel in the absence.

8. The method of claim 7, wherein the metabolite detected in subpart (c) is cyclic AMP.

9. The method of claim 7, each of the cells further comprising a recombinant expression construct encoding a cyclic AMP responsive element (CRE) transcription factor binding site operatively linked to a nucleic acid sequence encoding a protein capable of producing a detectable metabolite.

5

10. The method of claim 9, wherein the nucleic acid sequence encodes β -galactosidase.

11. The method of claim 9, wherein the recombinant expression construct is pCRE/ β -galactosidase.

10

12. The method of claim 9, wherein the detectable metabolite produced by the protein encoded by the recombinant expression construct is produced by binding of the test compound to the mammalian melanocortin receptor encoded by each of the cells of the panel.

15

13. The method of claim 1 wherein the test compound is an agonist of the MC-3 mammalian melanocortin receptor.

14. The method of claim 1 wherein the test compound is an agonist of the MC-4 mammalian melanocortin receptor.

20

15. The method of claim 3 wherein the test compound is an agonist of the MC-3 mammalian melanocortin receptor.

25

16. The method of claim 3 wherein the test compound is an agonist of the MC-4 mammalian melanocortin receptor.

17. The method of claim 7 wherein the test compound is an antagonist of the MC-3 mammalian melanocortin receptor.

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18. The method of claim 7 wherein the test compound is an antagonist of the MC-4 mammalian melanocortin receptor.

19. The method of claim 9 wherein the test compound is an antagonist of the MC-3 mammalian melanocortin receptor.

20. The method of claim 9 wherein the test compound is an antagonist of the MC-4 mammalian melanocortin receptor.

21. A mammalian melanocortin MC-3 receptor agonist according to claims 13 or 15.

22. A mammalian melanocortin MC-4 receptor agonist according to claims 14 or 16.

23. A mammalian melanocortin MC-3 receptor antagonist according to claims 17 or 19.

24. A mammalian melanocortin MC-4 receptor antagonist according to claims 18 or 20.

25. A method of inhibiting feeding behavior in an animal, the method comprising administering an effective amount of a mammalian melanocortin MC-3 or MC-4 receptor agonist according to claim 21.

26. A method of stimulating feeding behavior in an animal, the method comprising administering an effective amount of a mammalian melanocortin MC-3 or MC-4 receptor antagonist according to claim 24.

27. A method for characterizing a mammalian melanocortin MC-3 or MC-4 receptor agonist as an inhibitor of feeding behavior in an animal, the method comprising:

(a) providing food to an animal that has been deprived of food for at least 12 hours with or without administering to the animal a mammalian melanocortin MC-3 or MC-4 receptor agonist according to claim 25; and

5 (b) comparing the amount of food eaten by the animal with and without administration of the mammalian melanocortin MC-3 or MC-4 receptor agonist.

28. A method for characterizing a mammalian melanocortin MC-3 or MC-4 receptor antagonist as a stimulator of feeding behavior in an animal, the method comprising:

10 (a) providing food to an animal that has not been otherwise deprived of food for at least 12 hours, with or without administering to the animal a mammalian melanocortin MC-3 or MC-4 receptor antagonist according to claim 26 immediately prior to the onset of darkness or nighttime; and

15 (b) comparing the amount of food eaten by the animal with and without administration of the mammalian melanocortin MC-3 or MC-4 receptor antagonist.

29. A mammalian melanocortin MC-3 or MC-4 receptor agonist having the general formula:

20 A-B-C-D-E-F-G-amide

wherein A is Leu, Ile, Nle, Met, or substituted analogues thereof;

B is Asp, Glu, or substituted analogues thereof;

C is His or substituted analogues thereof;

D is D-Phe, D-Tyr or substituted analogues thereof;

25 E is Arg, Lys, homoArg, homoLys, or substituted analogues thereof;

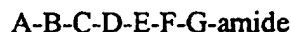
F is Trp or substituted analogues thereof;

G is Lys, homoLys or substituted analogues thereof;

and wherein the peptide is cyclized by the formation of an amide bond between the side chain carboxyl group of the Asp or Glu residue at position B in the peptide, and the side chain amino group of the Lys or homoLys residue at position G.

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30. A mammalian melanocortin MC-3 or MC-4 receptor antagonist having the general formula:



wherein A is Leu, Ile, Nle, Met, or substituted analogues thereof;

5 B is Asp, Glu or substituted analogues thereof;

C is His or substituted analogues thereof;

D is D-Nal or substituted analogues thereof;

E is Arg, Lys, homoArg, homoLys or substituted analogues thereof;

F is Trp or substituted analogues thereof;

10 G is Lys, homoLys or substituted analogues thereof;

and wherein the peptide is cyclized by the formation of an amide bond between the side chain carboxyl group of the Asp or Glu residue at position B in the peptide, and the side chain amino group of the Lys or homoLys residue at position G.

15 31. A biological screening panel for determining the receptor agonist/antagonist profile of a test compound, the panel comprising a first mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the α -MSH receptor, a second mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the ACTH receptor, a third mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-3 receptor, a fourth mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-4 receptor, and a fifth mammalian cell comprising a recombinant expression construct encoding a mammalian melanocortin receptor that is the MC-5 receptor, wherein each mammalian cell expresses the melanocortin receptor encoded by the recombinant expression construct comprising the cell.

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FIG. 1A

TTCCTGACAA	GACT	ATG	TCC	ACT	CAG	GAG	CCC	CAG	AAG	AGT	CTT	CTG	GGT	50		
		Met	Ser	Thr	Gln	Glu	Pro	Gln	Lys	Ser	Leu	Leu	Gly			
		1				5					10					
TCT	CTC	AAC	TCC	AAT	GCC	ACC	TCT	CAC	CTT	GGA	CTG	GCC	ACC	AAC	CAG	98
Ser	Leu	Asn	Ser	Asn	Ala	Thr	Ser	His	Leu	Gly	Leu	Ala	Thr	Asn	Gln	
		15				20					25					
TCA	GAG	CCT	TGG	TGC	CTG	TAT	GTG	TCC	ATC	CCA	GAT	GGC	CTC	TTC	CTC	146
Ser	Glu	Pro	Trp	Cys	Leu	Tyr	Val	Ser	Ile	Pro	Asp	Gly	Leu	Phe	Leu	
		30				35					40					
AGC	CTA	GGG	CTG	GTG	AGT	CTG	GTG	GAG	AAT	GTG	CTG	GTT	GTG	ATA	GCC	194
Ser	Leu	Gly	Leu	Val	Ser	Leu	Val	Glu	Asn	Val	Leu	Val	Val	Ile	Ala	
		45				50				55					60	
ATC	ACC	AAA	AAC	CGC	AAC	CTG	CAC	TCG	CCC	ATG	TAT	TAC	TTC	ATC	TGC	242
Ile	Thr	Lys	Asn	Arg	Asn	Leu	His	Ser	Pro	Met	Tyr	Tyr	Phe	Ile	Cys	
				65					70					75		
TGC	CTG	GCC	CTG	TCT	GAC	CTG	ATG	GTA	AGT	GTC	AGC	ATC	GTG	CTG	GAG	290
Cys	Leu	Ala	Leu	Ser	Asp	Leu	Met	Val	Ser	Val	Ser	Ile	Val	Leu	Glu	
			80					85					90			
ACT	ACT	ATC	ATC	CTG	CTG	CTG	GAG	GTG	GGC	ATC	CTG	GTG	GCC	AGA	GTG	338
Thr	Thr	Ile	Ile	Leu	Leu	Leu	Glu	Val	Gly	Ile	Leu	Val	Ala	Arg	Val	
		95				100					105					
GCT	TTG	GTG	CAG	CAG	CTG	GAC	AAC	CTC	ATT	GAC	GTG	CTC	ATC	TGT	GGC	386
Ala	Leu	Val	Gln	Gln	Leu	Asp	Asn	Leu	Ile	Asp	Val	Leu	Ile	Cys	Gly	
		110				115					120					
TCC	ATG	GTG	TCC	AGT	CTC	TGC	TTC	CTG	GGC	ATC	ATT	GCT	ATA	GAC	CGC	434
Ser	Met	Val	Ser	Ser	Leu	Cys	Phe	Leu	Gly	Ile	Ile	Ala	Ile	Asp	Arg	
		125				130				135					140	
TAC	ATC	TCC	ATC	TTC	TAT	GCG	CTG	CGT	TAT	CAC	AGC	ATC	GTG	ACG	CTG	482
Tyr	Ile	Ser	Ile	Phe	Tyr	Ala	Leu	Arg	Tyr	His	Ser	Ile	Val	Thr	Leu	
				145					150					155		
CCC	AGA	GCA	CGA	CGG	GCT	GTC	GTG	GGC	ATC	TGG	ATG	GTC	AGC	ATC	GTC	530
Pro	Arg	Ala	Arg	Arg	Ala	Val	Val	Gly	Ile	Trp	Met	Val	Ser	Ile	Val	
			160					165					170			

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FIG. 1B

TCC AGC ACC CTC TTT ATC ACC TAC TAC AAG CAC ACA GCC GTT CTG CTC Ser Ser Thr Leu Phe Ile Thr Tyr Tyr Lys His Thr Ala Val Leu Leu 175 180 185	578
TGC CTC GTC ACT TTC TTT CTA GCC ATG CTG GCA CTC ATG GCG ATT CTG Cys Leu Val Thr Phe Phe Leu Ala Met Leu Ala Leu Met Ala Ile Leu 190 195 200	626
TAT GCC CAC ATG TTC ACG AGA GCG TGC CAG CAC GTC CAG GGC ATT GCC Tyr Ala His Met Phe Thr Arg Ala Cys Gln His Val Gln Gly Ile Ala 205 210 215 220	674
CAG CTC CAC AAA AGG CCG CCG TCC ATC CGC CAA GGC TTC TGC CTC AAG Gln Leu His Lys Arg Arg Arg Ser Ile Arg Gln Gly Phe Cys Leu Lys 225 230 235	722
GGT GCT GCC ACC CTT ACT ATC CTT CTG GGG ATT TTC TTC CTG TGC TGG Gly Ala Ala Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp 240 245 250	770
GGC CCC TTC TTC CTG CAT CTC TTG CTC ATC GTC CTC TGC CCT CAG CAC Gly Pro Phe Phe Leu His Leu Leu Ile Val Leu Cys Pro Gln His 255 260 265	818
CCC ACC TGC AGC TGC ATC TTC AAG AAC TTC AAC CTC TTC CTC CTC CTC Pro Thr Cys Ser Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Leu Leu 270 275 280	866
ATC GTC CTC AGC TCC ACT GTT GAC CCC CTC ATC TAT GCT TTC CGC AGC Ile Val Leu Ser Ser Thr Val Asp Pro Leu Ile Tyr Ala Phe Arg Ser 285 290 295 300	914
CAG GAG CTC CGC ATG ACA CTC AAG GAG GTG CTG CTG TGC TCC TGG Gln Glu Leu Arg Met Thr Leu Lys Glu Val Leu Leu Cys Ser Trp 305 310 315	959
TGATCAGAGG GCGCTGGGCA GAGGGTGACA GTGATATCCA GTGGCCTGCA TCTGTGAGAC	1019
CACAGGTACT CATCCCTTCC TGATCTCCAT TTGTCTAAGG GTCGACAGGA TGAGCTTTAA	1079
AATAGAAACC CAGAGTGCCT GGGGCCAGGA GAAAGGGTAA CTGTGACTGC AGGGCTCACC	1139
CAGGGCAGCT ACGGGAAGTG GAGGAGACAG GGATGGGAAC TCTAGCCCTG AGCAAGGGTC	1199
AGACCACAGG CTCCTGAAGA GCTTCACCTC TCCCCACCTA CAGGCAACTC CTGCTCAAGC	1259
C	1260

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FIG. 2A

CCCGCATGTG	GCCGCCCTCA	ATGGAGGGCT	CTGAGAACGA	CTTTTAAAC	GCAGAGAAAA	60
AGCTCCATTC	TTCCAGACC	TCAGCGCAGC	CCTGGCCCAG	GAAGGGAGGA	GACAGAGGCC	120
AGGACGGTCC	AGAGGTGTCTG	AAATGTCTCTG	GGAACCTGAG	CAGCAGCCAC	CAGGGAAGAG	180
GCAGGGAGGG	AGCTGAGGAC	CAGGCTTGGT	TGTGAGAATC	CCTGAGCCCA	GGCGGTTGAT	240
GCCAGGAGGT	GTCTGGACTG	GCTGGGCCAT	GCCTGGGCTG	ACCTGTCCAG	CCAGGGAGAG	300
GGTGTGAGGG	CAGATCTGGG	GGTGCCCGA	TGGAAGGAGG	CAGGCATGGG	GACACCCAAG	360
GCCCCCTGGC	AGCACCATGA	ACTAAGCAGG	ACACCTGGAG	GGGAAGAACT	GTGGGGACCT	420
GGAGGCCTCC	AACGACTCCT	TCCTGCTTCC	TGGACAGGAC	T ATG GCT GTG CAG		473
				Met Ala Val Gln		
				1		
GGA TCC CAG AGA AGA CTT CTG GGC TCC CTC AAC TCC ACC CCC ACA GCC						521
Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser Thr Pro Thr Ala						
5 10 15 20						
ATC CCC CAG CTG GGG CTG GCT GCC AAC CAG ACA GGA GCC CGG TGC CTG						569
Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly Ala Arg Cys Leu						
25 30 35						
GAG GTG TCC ATC TCT GAC GGG CTC TTC CTC AGC CTG GGG CTG GTG AGC						617
Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu Gly Leu Val Ser						
40 45 50						
TTG GTG GAG AAC GCG CTG GTG GTG GCC ACC ATC GCC AAG AAC CGG AAC						665
Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala Lys Asn Arg Asn						
55 60 65						
CTG CAC TCA CCC ATG TAC TGC TTC ATC TGC TGC CTG GCC TTG TCG GAC						713
Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu Ala Leu Ser Asp						
70 75 80						
CTG CTG GTG AGC GGG ACG AAC GTG CTG GAG ACG GCC GTC ATC CTC CTG						761
Leu Leu Val Ser Gly Thr Asn Val Leu Glu Thr Ala Val Ile Leu Leu						
85 90 95 100						
CTG GAG GCC GGT GCA CTG GTG GCC CGG GCT GCG GTG CTG CAG CAG CTG						809
Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val Leu Gln Gln Leu						
105 110 115						
GAC AAT GTC ATT GAC GTG ATC ACC TGC AGC TCC ATG CTG TCC AGC CTC						857
Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met Leu Ser Ser Leu						
120 125 130						
TGC TTC CTG GGC GCC ATC GCC GTG GAC CGC TAC ATC TCC ATC TTC TAC						905
Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile Ser Ile Phe Tyr						
135 140 145						
GCA CTG CGC TAC CAC AGC ATC GTG ACC CTG CCG CGG GCG CCG CGA GCC						953
Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Pro Arg Ala						
150 155 160						

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FIG. 2B

GTT GCG GCC ATC TGG GTG GCC AGT GTC GTC TTC AGC ACG CTC TTC ATC Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser Thr Leu Phe Ile 165 170 175 180	1001
GCC TAC TAC GAC CAC GTG GCC GTC CTG CTG TGC CTC GTG GTC TTC TTC Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu Val Val Phe Phe 185 190 195	1049
CTG GCT ATG CTG GTG CTC ATG GCC GTG CTG TAC GTC CAC ATG CTG GCC Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val His Met Leu Ala 200 205 210	1097
CGG GCC TGC CAG CAC GCC CAG GGC ATC GCC CGG CTC CAC AAG AGG CAG Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu His Lys Arg Gln 215 220 225	1145
CGC CCG GTC CAC CAG GGC TTT GGC CTT AAA GGC GCT GTC ACC CTC ACC Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala Val Thr Leu Thr 230 235 240	1193
ATC CTG CTG GGC ATT TTC TTC CTC TGC TGG GGC CCC TTC TTC CTG CAT Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro Phe Phe Leu His 245 250 255 260	1241
CTC ACA CTC ATC GTC CTC TGC CCC GAG CAC CCC ACG TGC GGC TGC ATC Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr Cys Gly Cys Ile 265 270 275	1289
TTC AAG AAC TTC AAC CTC TTT CTC GCC CTC ATC ATC TGC AAT GCC ATC Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile Cys Asn Ala Ile 280 285 290	1337
ATC GAC CCC CTC ATC TAC GCC TTC CAC AGC CAG GAG CTC CGC AGG ACG Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu Leu Arg Arg Thr 295 300 305	1385
CTC AAG GAG GTG CTG ACA TGC TCC TGG TGAGCGCGGT GCACGCGCTT Leu Lys Glu Val Leu Thr Cys Ser Trp 310 315	1432
TAAGTGTGCT GGGCAGAGGG AGGTGGTGAT ATTGTGGTCT GTTTCCTGTG TGACCCTGGG	1492
CAGTTCCTTA CCTCCCTGGT CCCCGTTTGT CAAAGAGGAT GGACTAAATG ATCTCTGAAA	1552
GTGTTGAAGC GCGGACCCCTT CTGGGCAGGG AGGGGTCTTG CAAACTCCA GGCAGGACTT	1612
CTCACCAGCA GTCGTGGGAA C	1633

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FIG. 3A

ACAACACTTT ATATATATTT TTATAAATGT AAGGGGTACA AAGGTGCCAT TTTGTTACAT	60
GGATATACCG TGTAGTGGTG AAGCCTGGGC TTTTAGTGTA TCTGTCATCA GAATAACATA	120
CGTGTTACCC ATAGGAATTT CTCATCACCC GCCCCCTCCA CCCTTCGAGT CTCCAATGTC	180
CATTCCACAC TCTATATCCA CGTGATGCA TATAGCTCCA CATATAAGTG AGAACATGTA	240
GTATTGACT TCCTCTTCT GAGTTATTC ACTTTGATAA TGGCCTCCAC TTCCATCCAT	300
GTTGCTGCAA AAGACATGAC CTTATTCTTT TTGATAGCTG GGGAGTACTC CATTGTGTAT	360
ATGTACCACA TTTCTTTATC CATTACCCCA TTGAGAACAC TTAGTTGATT CCATATCTTT	420
GCTATTGTCA CTAGTGCTGC AATAACATA CATGTGCAGG CTCCTTCTAA TATACTGATT	480
TATATTTTAT GGAGAGAGAT AGAGTTCTTA GCGAGTGTGC TGTTTATTTT TAGTGTACTT	540
GCAACTAATA TTCTGTATAC TCCCTTTAGG TGATTGGAGA TTTAACTTAG ATCTCCAGCA	600
AGTGCTACAA GAAGAAAAGA TCCTGAAGAA TCAATCAAGT TTCCTGAAG TCAAGTCCAA	660
GTAACATCCC CGCCTTAACC ACAAGCAGGA GAA ATG AAG CAC ATT ATC AAC TCG	714
Met Lys His Ile Ile Asn Ser	
1 5	
TAT GAA AAC ATC AAC AAC ACA GCA AGA AAT AAT TCC GAC TGT CCT CGT	762
Tyr Glu Asn Ile Asn Asn Thr Ala Arg Asn Asn Ser Asp Cys Pro Arg	
10 15 20	
GTG GTT TTG CCG GAG GAG ATA TTT TTC ACA ATT TCC ATT GTT GGA GTT	810
Val Val Leu Pro Glu Glu Ile Phe Phe Thr Ile Ser Ile Val Gly Val	
25 30 35	
TTG GAG AAT CTG ATC GTC CTG CTG GCT GTG TTC AAG AAT AAG AAT CTC	858
Leu Glu Asn Leu Ile Val Leu Leu Ala Val Phe Lys Asn Lys Asn Leu	
40 45 50 55	
CAG GCA CCC ATG TAC TTT TTC ATC TGT AGC TTG GCC ATA TCT GAT ATG	906
Gln Ala Pro Met Tyr Phe Phe Ile Cys Ser Leu Ala Ile Ser Asp Met	
60 65 70	
CTG GGC AGC CTA TAT AAG ATC TTG GAA AAT ATC CTG ATC ATA TTG AGA	954
Leu Gly Ser Leu Tyr Lys Ile Leu Glu Asn Ile Leu Ile Ile Leu Arg	
75 80 85	
AAC ATG GGC TAT CTC AAG CCA CGT GGC AGT TTT GAA ACC ACA GCC GAT	1002
Asn Met Gly Tyr Leu Lys Pro Arg Gly Ser Phe Glu Thr Thr Ala Asp	
90 95 100	
GAC ATC ATC GAC TCC CTG TTT GTC CTC TCC CTG CTT GGC TCC ATC TTC	1050
Asp Ile Ile Asp Ser Leu Phe Val Leu Ser Leu Leu Gly Ser Ile Phe	
105 110 115	

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FIG. 3B

AGC CTG TCT GTG ATT GCT GCG GAC CGC TAC ATC ACC ATC TTC CAC GCA Ser Leu Ser Val Ile Ala Ala Asp Arg Tyr Ile Thr Ile Phe His Ala 120 125 130 135	1098
CTG CGG TAC CAC AGC ATC GTG ACC ATG CGC CGC ACT GTG GTG GTG CTT Leu Arg Tyr His Ser Ile Val Thr Met Arg Arg Thr Val Val Val Leu 140 145 150	1146
ACG GTC ATC TGG ACG TTC TGC ACG GGG ACT GGC ATC ACC ATG GTG ATC Thr Val Ile Trp Thr Phe Cys Thr Gly Thr Gly Ile Thr Met Val Ile 155 160 165	1194
TTC TCC CAT CAT GTG CCC ACA GTG ATC ACC TTC ACG TCG CTG TTC CCG Phe Ser His His Val Pro Thr Val Ile Thr Phe Thr Ser Leu Phe Pro 170 175 180	1242
CTG ATG CTG GTC TTC ATC CTG TGC CTC TAT GTG CAC ATG TTC CTG CTG Leu Met Leu Val Phe Ile Leu Cys Leu Tyr Val His Met Phe Leu Leu 185 190 195	1290
GCT CGA TCC CAC ACC AGG AAG ATC TCC ACC CTC CCC AGA GCC AAC ATG Ala Arg Ser His Thr Arg Lys Ile Ser Thr Leu Pro Arg Ala Asn Met 200 205 210 215	1338
AAA GGG GCC ATC ACA CTG ACC ATC CTG CTC GGG GTC TTC ATC TTC TGC Lys Gly Ala Ile Thr Leu Thr Ile Leu Leu Gly Val Phe Ile Phe Cys 220 225 230	1386
TGG GCC CCC TTT GTG CTT CAT GTC CTC TTG ATG ACA TTC TGC CCA AGT Trp Ala Pro Phe Val Leu His Val Leu Leu Met Thr Phe Cys Pro Ser 235 240 245	1434
AAC CCC TAC TGC GCC TGC TAC ATG TCT CTC TTC CAG GTG AAC GGC ATG Asn Pro Tyr Cys Ala Cys Tyr Met Ser Leu Phe Gln Val Asn Gly Met 250 255 260	1482
TTG ATC ATG TGC AAT GCC GTC ATT GAC CCC TTC ATA TAT GCC TTC CGG Leu Ile Met Cys Asn Ala Val Ile Asp Pro Phe Ile Tyr Ala Phe Arg 265 270 275	1530
AGC CCA GAG CTC AGG GAC GCA TTC AAA AAG ATG ATC TTC TGC AGC AGG Ser Pro Glu Leu Arg Asp Ala Phe Lys Lys Met Ile Phe Cys Ser Arg 280 285 290 295	1578
TAC TGG TAGAATGGCT GATCCCTGGT TTTAGAATCC ATGGGAATAA CGTTGCCAAG Tyr Trp	1634
TGCCAGAATA GTGTAACATT CCAACAAATG CCAGTGCTCC TCACTGGCCT TCCTTCCCTA ATGGATGCAA GGATGACCCA CCAGCTAGTG TTTCTGAATA CTATGGCCAG GAACAGTCTA TTGTAGGGGC AACTCTATTT GTGACTGGAC AGATAAAACG TGTAGTAAAA GAAGGATAGA ATACAAAGTA TTAGGTACAA AAGTAATTAG GTTTGCATTA CTTATGACAA ATGCATTACT TTTGACACCA TCTAGTAAAA CAGCAATAAA AATTCAAGGG CTTTGGGCTA AGGCAAGAC TTGCTTTCTT GTGGACATTA ACAAGCCAGT TCTGAGGCGG CCTTTCAGG TGGAGGCCAT TGCAGCCAAT TTCAGAGT	1694 1754 1814 1874 1934 1994 2012

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FIG. 4A

GGGCCAGAA AGTTCTGCT TCAGAGCAGA AGATCTTCAG CAAGAACTAC AAAGAAGAAA	60
AGATTCTGGA GAATCAATCA AGTTTCTGT CAAGTTCCAG TAACGTTTCT GTCTTAACTG	120
CACACAGGAA AG ATG AAA CAC ATT CTC AAT CTG TAT GAA AAC ATC AAC Met Lys His Ile Leu Asn Leu Tyr Glu Asn Ile Asn 1 5 10	168
AGT ACA GCA AGA AAT AAC TCA GAC TGT CCT GCT GTG ATT TTG CCA GAA Ser Thr Ala Arg Asn Asn Ser Asp Cys Pro Ala Val Ile Leu Pro Glu 15 20 25	216
GAG ATA TTT TTC ACA GTA TCC ATT GTT GGG GTT TTG GAG AAC CTG ATG Glu Ile Phe Phe Thr Val Ser Ile Val Gly Val Leu Glu Asn Leu Met 30 35 40	264
GTC CTT CTG GCT GTG GCC AAG AAT AAG AGT CTT CAG TCG CCC ATG TAC Val Leu Leu Ala Val Ala Lys Asn Lys Ser Leu Gln Ser Pro Met Tyr 45 50 55 60	312
TTT TTC ATC TGC AGC TTG GCT ATT TCC GAT ATG CTG GGG AGC CTG TAC Phe Phe Ile Cys Ser Leu Ala Ile Ser Asp Met Leu Gly Ser Leu Tyr 65 70 75	360
AAG ATT TTG GAA AAC GTT CTG ATC ATG TTC AAA AAC ATG GGT TAC CTC Lys Ile Leu Glu Asn Val Leu Ile Met Phe Lys Asn Met Gly Tyr Leu 80 85 90	408
GAG CCT CGA GGC AGT TTT GAA AGC ACA GCA GAT GAT GTG GTG GAC TCC Glu Pro Arg Gly Ser Phe Glu Ser Thr Ala Asp Asp Val Val Asp Ser 95 100 105	456
CTG TTC ATC CTC TCC CTT CTC GGC TCC ATC TGC AGC CTG TCT GTG ATT Leu Phe Ile Leu Ser Leu Leu Gly Ser Ile Cys Ser Leu Ser Val Ile 110 115 120	504
GCC GCT GAC CGC TAC ATC ACA ATC TTC CAC GCT CTG CAG TAC CAC CGC Ala Ala Asp Arg Tyr Ile Thr Ile Phe His Ala Leu Gln Tyr His Arg 125 130 135 140	552
ATC ATG ACC CCC GCA CCG TGC CCT CGT CAT CTG ACG GTC CTC TGG GCA Ile Met Thr Pro Ala Pro Cys Pro Arg His Leu Thr Val Leu Trp Ala 145 150 155	600
GGC TGC ACA GGC AGT GGC ATT ACC ATC GTG ACC TTC TCC CAT CAC GTC Gly Cys Thr Gly Ser Gly Ile Thr Ile Val Thr Phe Ser His His Val 160 165 170	648
CCC ACA GTG ATC GCC TTC ACA GCG CTG TTC CCG CTG ATG CTG GCC TTC Pro Thr Val Ile Ala Phe Thr Ala Leu Phe Pro Leu Met Leu Ala Phe 175 180 185	696
ATC CTG TGC CTC TAC GTG CAC ATG TTC CTG CTG GCC CGC TCC CAC ACC Ile Leu Cys Leu Tyr Val His Met Phe Leu Leu Ala Arg Ser His Thr 190 195 200	744
AGG AGG ACC CCC TCC CTT CCC AAA GCC AAC ATG AGA GGG GCC GTC ACA Arg Arg Thr Pro Ser Leu Pro Lys Ala Asn Met Arg Gly Ala Val Thr 205 210 215 220	792

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FIG. 4B

CTG ACT GTC CTG CTC GGG GTC TTC ATT TTC TGT TGG GCA CCC TTT GTC Leu Thr Val Leu Leu Gly Val Phe Ile Phe Cys Trp Ala Pro Phe Val 225 230 235	840
CTT CAT GTC CTC TTG ATG ACA TTC TGC CCA GCT GAC CCC TAC TGT GCC Leu His Val Leu Leu Met Thr Phe Cys Pro Ala Asp Pro Tyr Cys Ala 240 245 250	888
TGC TAC ATG TCC CTC TTC CAG GTG AAT GGT GTG TTG ATC ATG TGT AAT Cys Tyr Met Ser Leu Phe Gln Val Asn Gly Val Leu Ile Met Cys Asn 255 260 265	936
GCC ATC ATC GAC CCC TTC ATA TAT GCC TTT CGG AGC CCA GAG CTC AGG Ala Ile Ile Asp Pro Phe Ile Tyr Ala Phe Arg Ser Pro Glu Leu Arg 270 275 280	984
GTC GCA TTC AAA AAG ATG GTT ATC TGC AAC TGT TAC CAG TAGAATGATT Val Ala Phe Lys Lys Met Val Ile Cys Asn Cys Tyr Gln 285 290 295	1033
GGTCCCTGAT TTTAGGAGCC ACAGGGATAT ACTGTCAGGG ACAGAGTAGC GTGACAGACC	1093
AACAACACTA GGACT	1108

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FIG. 5A

GGCTGTAAC	GTAGCAACCG	GTGTTGGGTG	GGGATGAGAA	GAGACCAGAG	AGAGAGAGGG	60
TCAGAGCGAC	AGGGGATGAG	ACAGGCTGGT	CAGAGTCTGC	ACTGATTGTT	GGAGACGCAA	120
AGGAAAGTTT	TTTCTATGTC	TCCAACCTCC	CCCTCCTCCC	CCGTTTCTCT	CTGGAGAAAC	180
TAAATCTAG	ACTGGACAGC	ATCCACAAGA	GAAGCACCTA	GAAGAAGATT	TTTTTTTCCC	240
AGCAGCTTGC	TCAGGACCCCT	GCAGGAGCTG	CAGCCGGAAC	TGGTCCC GCC	GATAACC	297
ATG AAC TCT TCC TGC TGC CCG TCC TCC TCT TAT CCG ACG CTG CCT AAC	Met Asn Ser Ser Cys Cys Pro Ser Ser Ser Tyr Pro Thr Leu Pro Asn	1 5 10 15				345
CTC TCC CAG CAC CCT GCA GCC CCC TCT GCC AGC AAC CCG AGT GGC AGT	Leu Ser Gln His Pro Ala Ala Pro Ser Ala Ser Asn Arg Ser Gly Ser	20 25 30				393
GGG TTC TGC GAG CAG GTT TTC ATC AAG CCA GAG GTC TTC CTG GCA CTG	Gly Phe Cys Glu Gln Val Phe Ile Lys Pro Glu Val Phe Leu Ala Leu	35 40 45				441
GGC ATC GTC AGT CTG ATG GAA AAC ATC CTG GTG ATC CTG GCT GTG GTG	Gly Ile Val Ser Leu Met Glu Asn Ile Leu Val Ile Leu Ala Val Val	50 55 60				489
AGG AAC GGC AAC CTG CAC TCC CCC ATG TAC TTC TTC CTG CTG AGC CTG	Arg Asn Gly Asn Leu His Ser Pro Met Tyr Phe Phe Leu Leu Ser Leu	65 70 75 80				537
CTG CAG GCC GAC ATG CTG GTG AGC CTG TCC AAC TCC CTG GAG ACC ATC	Leu Gln Ala Asp Met Leu Val Ser Leu Ser Asn Ser Leu Glu Thr Ile	85 90 95				585
ATG ATC GTG GTT ATC AAC AGC GAC TCC CTG ACC TTG GAG GAC CAA TTC	Met Ile Val Val Ile Asn Ser Asp Ser Leu Thr Leu Glu Asp Gln Phe	100 105 110				633
ATC CAG CAC ATG GAC AAC ATC TTC GAC TCT ATG ATC TGC ATC TCC CTG	Ile Gln His Met Asp Asn Ile Phe Asp Ser Met Ile Cys Ile Ser Leu	115 120 125				681
GTG GCC TCC ATC TGC AAC CTC CTG GCC ATC GCC GTG GAC AGG TAC GTC	Val Ala Ser Ile Cys Asn Leu Leu Ala Ile Ala Val Asp Arg Tyr Val	130 135 140				729
ACC ATC TTC TAT GCC CTC CGT TAC CAC AGC ATC ATG ACG GTT AGG AAA	Thr Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Met Thr Val Arg Lys	145 150 155 160				777
GCC CTC TCC TTG ATC GTG GCC ATC TGG GTC TGC TOT GGC ATC TGC GGC	Ala Leu Ser Leu Ile Val Ala Ile Trp Val Cys Cys Gly Ile Cys Gly	165 170 175				825
GTG ATG TTC ATC GTC TAC TCC GAG AGC AAG ATG GTC ATC GTG TGC CTC	Val Met Phe Ile Val Tyr Ser Glu Ser Lys Met Val Ile Val Cys Leu	180 185 190				873

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FIG. 5B

ATC	ACC	ATG	TTC	TTC	GCC	ATG	GTG	CTC	CTC	ATG	GGC	ACC	CTG	TAC	ATC	921	
Ile	Thr	Met	Phe	Phe	Ala	Met	Val	Leu	Leu	Met	Gly	Thr	Leu	Tyr	Ile		
		195					200					205					
CAC	ATG	TTC	CTC	TTC	GCC	AGG	CTG	CAC	GTC	CAG	CGC	ATC	GCG	GCA	CTG	969	
His	Met	Phe	Leu	Phe	Ala	Arg	Leu	His	Val	Gln	Arg	Ile	Ala	Ala	Leu		
		210				215					220						
CCA	CCT	GCT	GAC	GGG	GTA	GCC	CCG	CAG	CAG	CAC	TGG	TGC	ATG	AAG	GGG	1017	
Pro	Pro	Ala	Asp	Gly	Val	Ala	Pro	Gln	Gln	His	Ser	Cys	Met	Lys	Gly		
225					230					235					240		
GCC	GTC	ACC	ATC	ACC	ATC	CTG	CTG	GGG	GTT	TTC	ATC	TTC	TGC	TGG	GCG	1065	
Ala	Val	Thr	Ile	Thr	Ile	Leu	Leu	Gly	Val	Phe	Ile	Phe	Cys	Trp	Ala		
				245				250						255			
CCT	TTC	TTC	CTC	CAC	CTG	GTC	CTC	ATC	ATC	ACC	TGC	CCC	ACC	AAC	CCC	1113	
Pro	Phe	Phe	Leu	His	Leu	Val	Leu	Ile	Ile	Thr	Cys	Pro	Thr	Asn	Pro		
			260					265					270				
TAC	TGC	ATC	TGC	TAC	ACG	GCG	CAC	TTC	AAC	ACC	TAC	CTG	GTT	CTC	ATC	1161	
Tyr	Cys	Ile	Cys	Tyr	Thr	Ala	His	Phe	Asn	Thr	Tyr	Leu	Val	Leu	Ile		
		275					280					285					
ATG	TGC	AAC	TCT	GTC	ATC	GAC	CCC	CTC	ATC	TAC	GCC	TTC	CGC	AGC	CTG	1209	
Met	Cys	Asn	Ser	Val	Ile	Asp	Pro	Leu	Ile	Tyr	Ala	Phe	Arg	Ser	Leu		
		290				295					300						
GAG	CTG	CGA	AAC	ACC	TTC	AAG	GAG	ATT	CTC	TGC	GGT	TGC	AAT	GGC	ATG	1257	
Glu	Leu	Arg	Asn	Thr	Phe	Lys	Glu	Ile	Leu	Cys	Gly	Cys	Asn	Gly	Met		
305					310					315					320		
AAC	GTG	GGC	TAGGAACCCC				CGAGGAGGTG				TTCCACGGCT				AGCCAAGAGA		1306
Asn	Val	Gly															
GAAAAGCAAT GCTCAGGTGA GACACAGAAG GG																1338	

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FIG. 6A

AGCTTCCGAG AGGCAGCCGA TGTGAGCATG TGCACACAGA TTCGTCTCCC AATGGCATGG	60
CAGCTTCAAG GAAAATTATT TTGAACAGAC TTGAATGCAT AAGATTAAAG TTAAAGCAGA	120
AGTGAGAACA AGAAAGCAAA GAGCAGACTC TTTCAACTGA GAATGAATAT TTTGAAGCCC	180
AAGATTTTAA AGTGATGATG ATTAGAGTCG TACCTAAAAG AGACTAAAAA CTCCATGTCA	240
AGCTCTGGAC TTGTGACATT TACTCACAGC AGGCATGGCA ATTTAGCCT CACAACCTTC	300
AGACAGATAA AGACTTGGAG GAAATAACTG AGACGACTCC CTGACCCAGG AGGTAAATC	360
AATTCAGGGG GACACTGGAA TTCTCCTGCC AGC ATG GTG AAC TCC ACC CAC CGT	414
Met Val Asn Ser Thr His Arg	
1 5	
GGG ATG CAC ACT TCT CTG CAC CTC TGG AAC CGC AGC AGT TAC AGA CTG	462
Gly Met His Thr Ser Leu His Leu Trp Asn Arg Ser Ser Tyr Arg Leu	
10 15 20	
CAC AGC AAT GCC AGT GAG TCC CTT GGA AAA GGC TAC TCT GAT GGA GGG	510
His Ser Asn Ala Ser Glu Ser Leu Gly Lys Gly Tyr Ser Asp Gly Gly	
25 30 35	
TGC TAC GAG CAA CTT TTT GTC TCT CCT GAG GTG TTT GTG ACT CTG GGT	558
Cys Tyr Glu Gln Leu Phe Val Ser Pro Glu Val Phe Val Thr Leu Gly	
40 45 50 55	
GTG ATC AGC TTG TTG GAG AAT ATC TTA GTG ATT GTG GCA ATA GCC AAG	606
Val Ile Ser Leu Leu Glu Asn Ile Leu Val Ile Val Ala Ile Ala Lys	
60 65 70	
AAC AAG AAT CTG CAT TCA CCC ATG TAC TTT TTC ATC TGC AGC TTG GCT	654
Asn Lys Asn Leu His Ser Pro Met Tyr Phe Phe Ile Cys Ser Leu Ala	
75 80 85	
GTG GCT GAT ATG CTG GTG AGC GTT TCA AAT GGA TCA GAA ACC ATT ATC	702
Val Ala Asp Met Leu Val Ser Val Ser Asn Gly Ser Glu Thr Ile Ile	
90 95 100	
ATC ACC CTA TTA AAC AGT ACA GAT ACG GAT GCA CAG AGT TTC ACA GTG	750
Ile Thr Leu Leu Asn Ser Thr Asp Thr Asp Ala Gln Ser Phe Thr Val	
105 110 115	
AAT ATT GAT AAT GTC ATT GAC TCG GTG ATC TGT AGC TCC TTG CTT GCA	798
Asn Ile Asp Asn Val Ile Asp Ser Val Ile Cys Ser Ser Leu Leu Ala	
120 125 130 135	
TCC ATT TGC AGC CTG CTT TCA ATT GCA GTG GAC AGG TAC TTT ACT ATC	846
Ser Ile Cys Ser Leu Leu Ser Ile Ala Val Asp Arg Tyr Phe Thr Ile	
140 145 150	
TTC TAT GCT CTC CAG TAC CAT AAC ATT ATG ACA GTT AAG CGG GTT GGG	894
Phe Tyr Ala Leu Gln Tyr His Asn Ile Met Thr Val Lys Arg Val Gly	
155 160 165	
ATC AGC ATA AGT TGT ATC TGG GCA GCT TGC ACG GTT TCA GGC ATT TTG	942
Ile Ser Ile Ser Cys Ile Trp Ala Ala Cys Thr Val Ser Gly Ile Leu	
170 175 180	

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FIG. 6B

TTC ATC ATT TAC TCA GAT AGT AGT GCT GTC ATC ATC TGC CTC ATC ACC Phe Ile Ile Tyr Ser Asp Ser Ser Ala Val Ile Ile Cys Leu Ile Thr 185 190 195	990
ATG TTC TTC ACC ATG CTG GCT CTC ATG GCT TCT CTC TAT GTC CAC CTG Met Phe Phe Thr Met Leu Ala Leu Met Ala Ser Leu Tyr Val His Leu 200 205 210 215	1038
TTC CTG ATG GCC AGG CTT CAC ATT AAG AGG ATT GCT GTC CTC CCC GGC Phe Leu Met Ala Arg Leu His Ile Lys Arg Ile Ala Val Leu Pro Gly 220 225 230	1086
ACT GGT GCC ATC CGC CAA GGT GCC AAT ATG AAG GGA GCG ATT ACC TTG Thr Gly Ala Ile Arg Gln Gly Ala Asn Met Lys Gly Ala Ile Thr Leu 235 240 245	1134
ACC ATC CTG ATT GGC GTC TTT GTT GTC TGC TGG GCC CCA TTC TTC CTC Thr Ile Leu Ile Gly Val Phe Val Val Cys Trp Ala Pro Phe Phe Leu 250 255 260	1182
CAC TTA ATA TTC TAC ATC TCT TGT CCT CAG AAT CCA TAT TGT GTG TGC His Leu Ile Phe Tyr Ile Ser Cys Pro Gln Asn Pro Tyr Cys Val Cys 265 270 275	1230
TTC ATG TCT CAC TTT AAC TTG TAT CTC ATA CTG ATC ATG TGT AAT TCA Phe Met Ser His Phe Asn Leu Tyr Leu Ile Leu Ile Met Cys Asn Ser 280 285 290 295	1278
ATC ATC GAT CCT CTG ATT TAT GCA CTC CGG AGT CAA GAA CTG AGG AAA Ile Ile Asp Pro Leu Ile Tyr Ala Leu Arg Ser Gln Glu Leu Arg Lys 300 305 310	1326
ACC TTC AAA GAG ATC ATC TCT TCC TAT CCC CTG GGA GGC CTT TGT GAC Thr Phe Lys Glu Ile Ile Ser Ser Tyr Pro Leu Gly Gly Leu Cys Asp 315 320 325	1374
TTG TCT AGC AGA TAT TAAATGGGGA CAGAGCACGC AATATAGGAA CATCCATAAG Leu Ser Ser Arg Tyr 330	1429
AGACTTTTTC ACTCTTACCC TACCTGAATA TTCTACTTCT GCAACAGCTT TCTCTCCGT	1489
GTAGGGTACT GGTGAGATA TCCATTGTGT AAATTTAAGC CTATGATTTT TAATGAGAAA	1549
AAATGCCCAG TCTCTGTATT ATTTCCAATC TCATGCTACT TTTTGGCCA TAAATATGA	1609
ATCTATGTTA TAGGTTOTAG GCACTGTGGA TTTACAAAAA GAAAAGTCCT TATTAAAAGC	1669
TT	1671

FIG. 7A

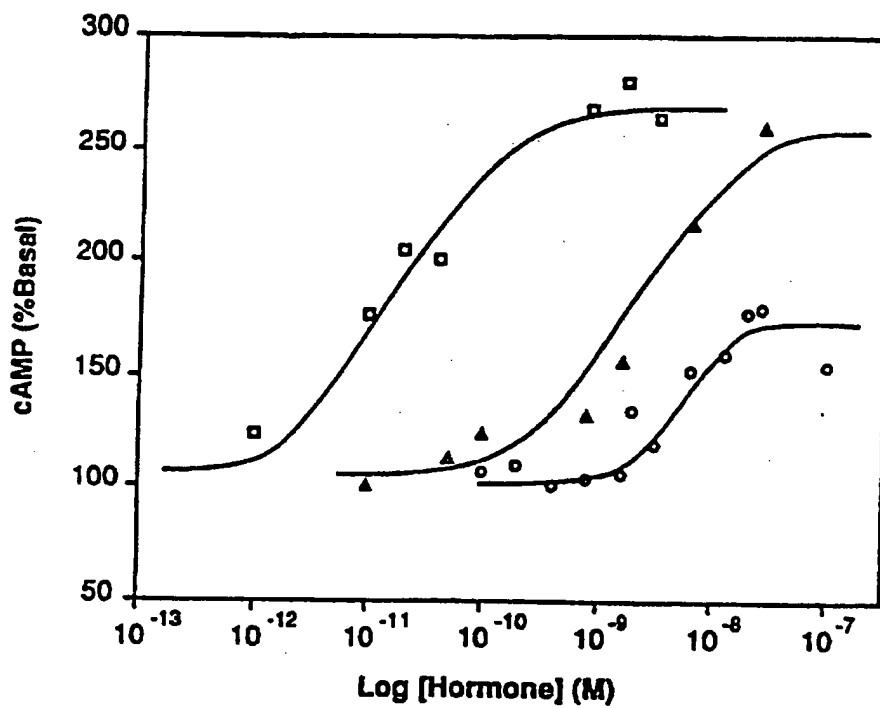
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TCA GAG GAT GGC ATT TTA GGA TCA AAT GTC AAG AAC AAG TCT TTG GCC Ser Glu Asp Gly Ile Leu Gly Ser Asn Val Lys Asn Lys Ser Leu Ala 20 25 30	96
TGT GAA GAA ATG GGC ATT GCC GTG GAG GTG TTC CTG ACC CTG GGT CTC Cys Glu Glu Met Gly Ile Ala Val Glu Val Phe Leu Thr Leu Gly Leu 35 40 45	144
GTC AGC CTC TTA GAG AAC ATC CTG GTC ATT GGG GCC ATA GTA AAG AAC Val Ser Leu Leu Glu Asn Ile Leu Val Ile Gly Ala Ile Val Lys Asn 50 55 60	192
AAA AAC CTG CAC TCA CCC ATG TAC TTC TTT GTG GGC AGC TTA GCC GTG Lys Asn Leu His Ser Pro Met Tyr Phe Phe Val Gly Ser Leu Ala Val 65 70 75 80	240
GCC GAC ATG CTG GTG AGC ATG TCC AAT GCC TGG GAG ACT GTC ACC ATA Ala Asp Met Leu Val Ser Met Ser Asn Ala Trp Glu Thr Val Thr Ile 85 90 95	288
TAC TTG CTA AAT AAT AAA CAC CTG GTG ATA GCC GAC ACC TTT GTG CGA Tyr Leu Leu Asn Asn Lys His Leu Val Ile Ala Asp Thr Phe Val Arg 100 105 110	336
CAC ATC GAC AAC GTG TTC GAC TCC ATG ATC TGC ATC TCT GTG GTG GCC His Ile Asp Asn Val Phe Asp Ser Met Ile Cys Ile Ser Val Val Ala 115 120 125	384
TCG ATG TGC AGT TTG CTG GCC ATT GCG GTG GAT AGG TAC ATC ACC ATC Ser Met Cys Ser Leu Leu Ala Ile Ala Val Asp Arg Tyr Ile Thr Ile 130 135 140	432
TTC TAT GCC TTG CGC TAC CAC CAC ATC ATG ACC GCG AGG CGC TCG GGG Phe Tyr Ala Leu Arg Tyr His His Ile Met Thr Ala Arg Arg Ser Gly 145 150 155 160	480
GTG ATC ATC GCC TGC ATT TGG ACC TTC TGC ATA AGC TGC GGC ATT GTT Val Ile Ile Ala Cys Ile Trp Thr Phe Cys Ile Ser Cys Gly Ile Val 165 170 175	528
TTC ATC ATC TAC TAT GAG TCC AAG TAT GTG ATC ATT TGC CTC ATC TCC Phe Ile Ile Tyr Tyr Glu Ser Lys Tyr Val Ile Ile Cys Leu Ile Ser 180 185 190	576
ATG TTC TTC ACC ATG CTG TTC TTC ATG GTG TCT CTG TAT ATA CAC ATG Met Phe Phe Thr Met Leu Phe Phe Met Val Ser Leu Tyr Ile His Met 195 200 205	624
TTC CTC CTG GCC CGG AAC CAT GTC AAG CGG ATA GCA GCT TCC CCC AGA Phe Leu Leu Ala Arg Asn His Val Lys Arg Ile Ala Ala Ser Pro Arg 210 215 220	672
TAC AAC TCC GTG AGG CAA AGG ACC AGC ATG AAG GGG GCT ATT ACC CTC Tyr Asn Ser Val Arg Gln Arg Thr Ser Met Lys Gly Ala Ile Thr Leu 225 230 235 240	720

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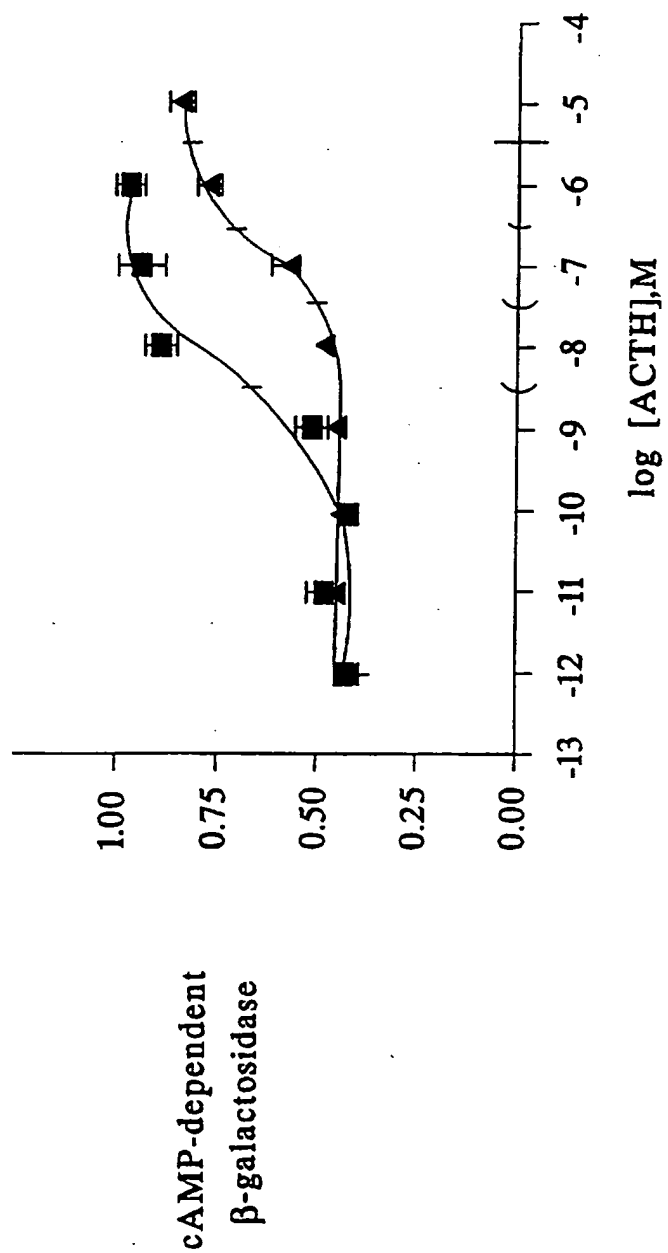
FIG. 7B

ACC	ATG	CTA	CTG	GGG	ATT	TTC	ATT	OTC	TGC	TGG	TCT	CCC	TTC	TTT	CTT	768
Thr	Met	Leu	Leu	Gly	Ile	Phe	Ile	Val	Cys	Trp	Ser	Pro	Phe	Phe	Leu	
				245					250					255		
CAC	CTT	ATC	TTA	ATG	ATC	TCC	TGC	CCT	CAG	AAC	GTC	TAC	TGC	TCT	TGC	816
His	Leu	Ile	Leu	Met	Ile	Ser	Cys	Pro	Gln	Asn	Val	Tyr	Cys	Ser	Cys	
			260					265					270			
TTT	ATG	TCT	TAC	TTC	AAC	ATG	TAC	CTT	ATA	CTC	ATC	ATG	TGC	AAC	TCC	864
Phe	Met	Ser	Tyr	Phe	Asn	Met	Tyr	Leu	Ile	Leu	Ile	Met	Cys	Asn	Ser	
		275					280					285				
GTG	ATC	GAT	CCT	CTC	ATC	TAC	GCC	CTC	CGC	AGC	CAA	GAG	ATG	CGG	AGG	912
Val	Ile	Asp	Pro	Leu	Ile	Tyr	Ala	Leu	Arg	Ser	Gln	Glu	Met	Arg	Arg	
	290					295					300					
ACC	TTT	AAG	GAG	ATC	GTC	TGT	TGT	CAC	GGA	TTC	CGG	CGA	CCT	TGT	AGG	960
Thr	Phe	Lys	Glu	Ile	Val	Cys	Cys	His	Gly	Phe	Arg	Arg	Pro	Cys	Arg	
305					310					315					320	
CTC	CTT	GGC	GGG	TAT	TAA											978
Leu	Leu	Gly	Gly	Tyr	*											
				325												

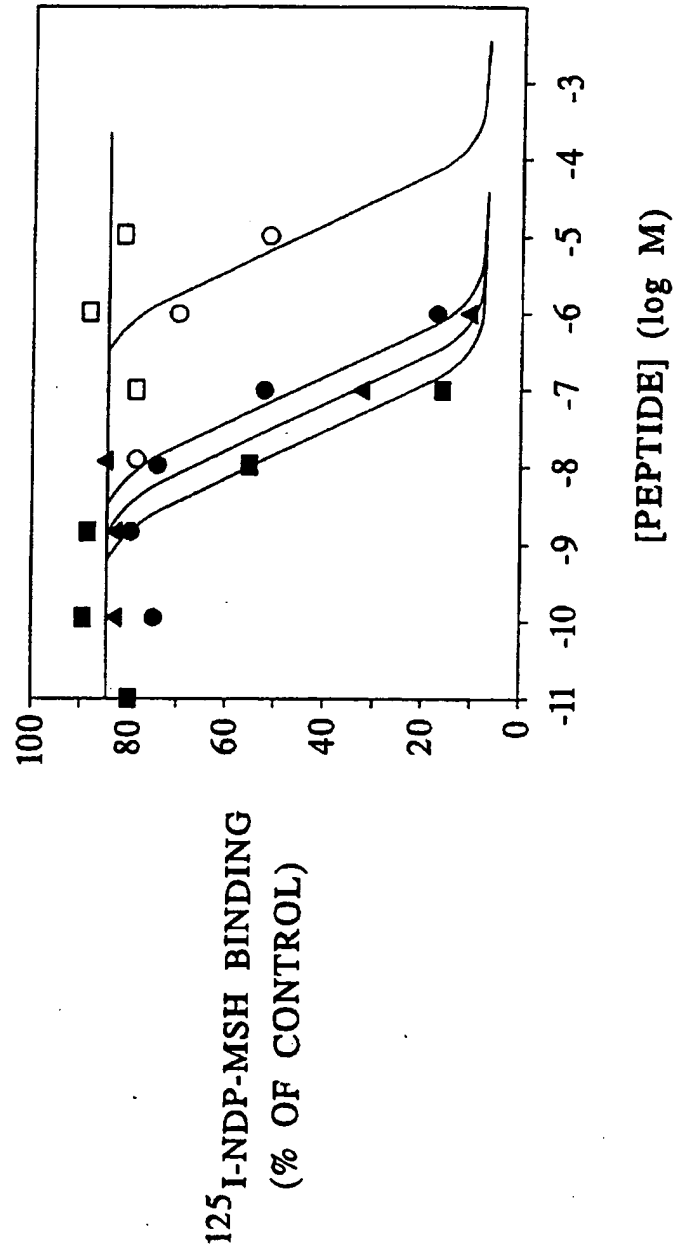
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FIG. 8

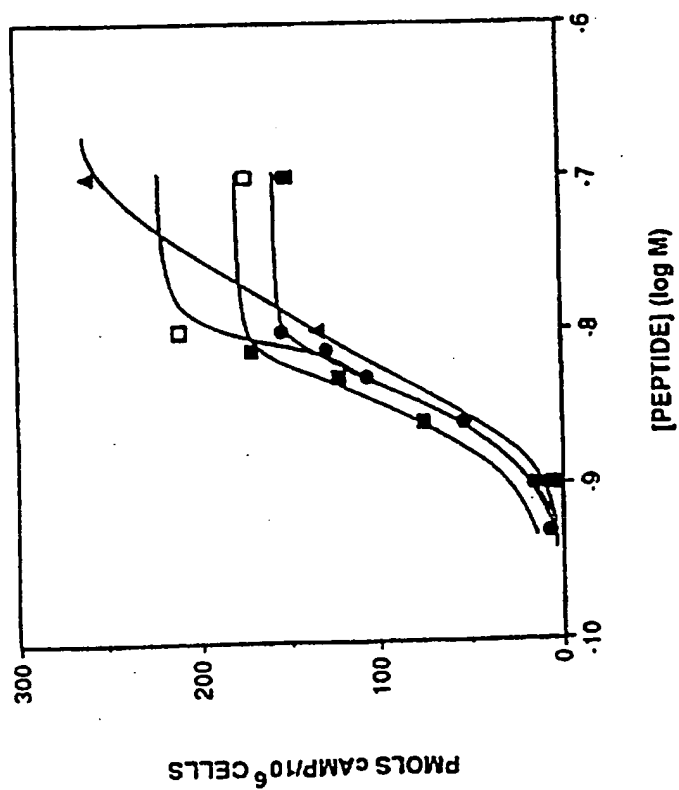
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FIG. 9

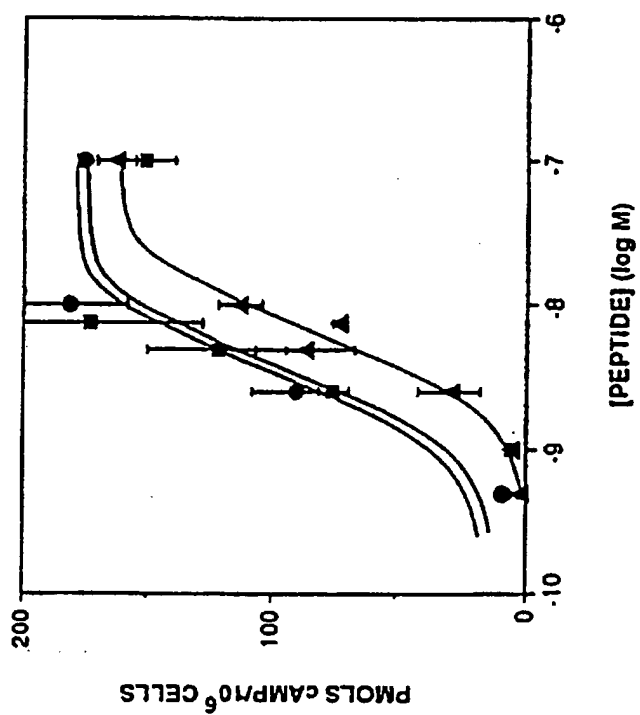
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FIG. 10

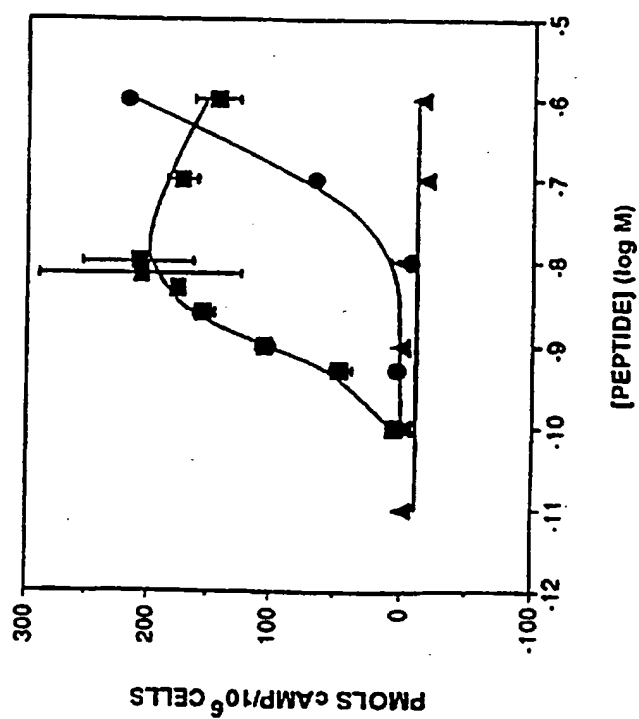
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FIG. 11A

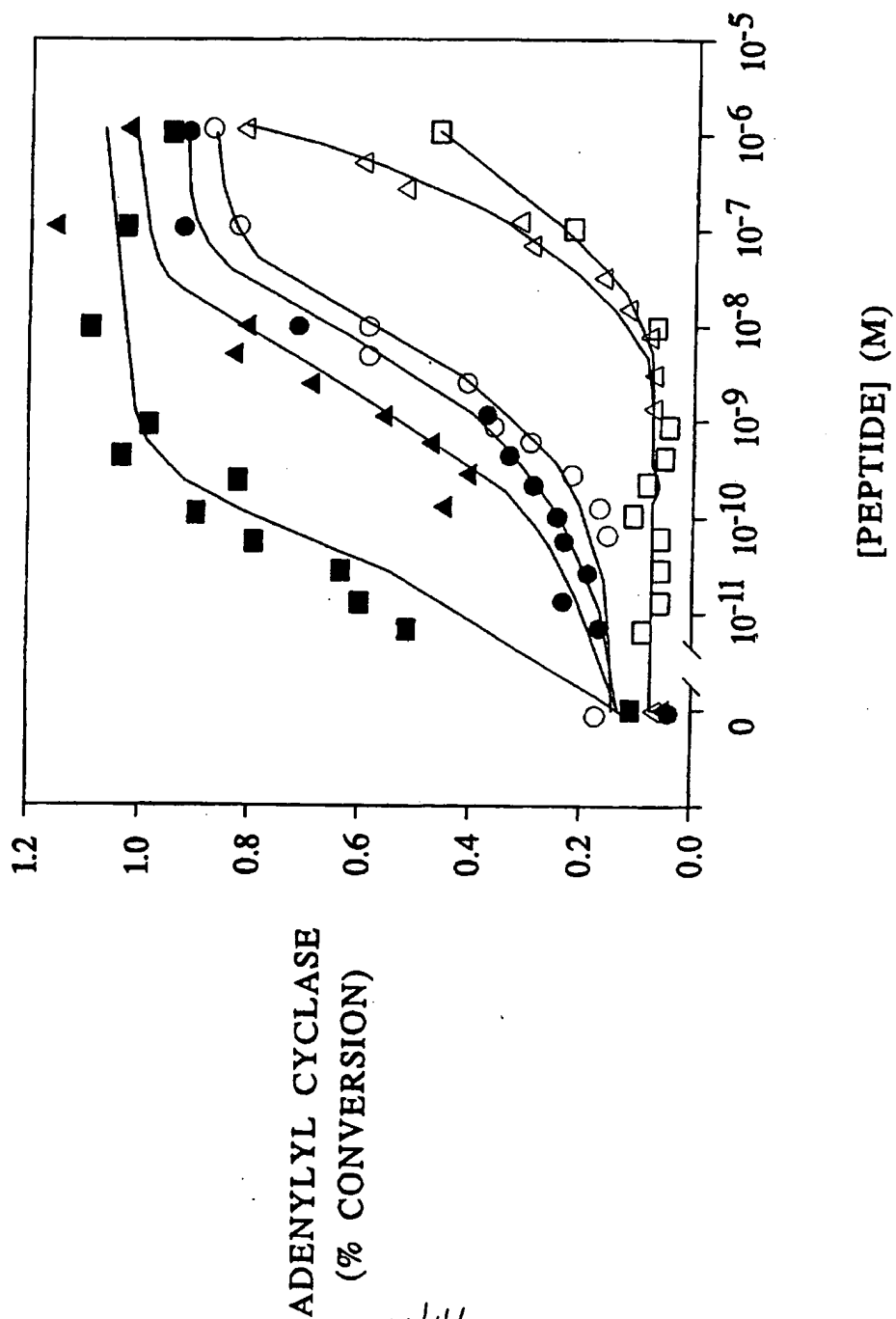
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FIG. 11B

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FIG. 11C

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FIG. 12

ADENYLYL CYCLASE
(% CONVERSION)

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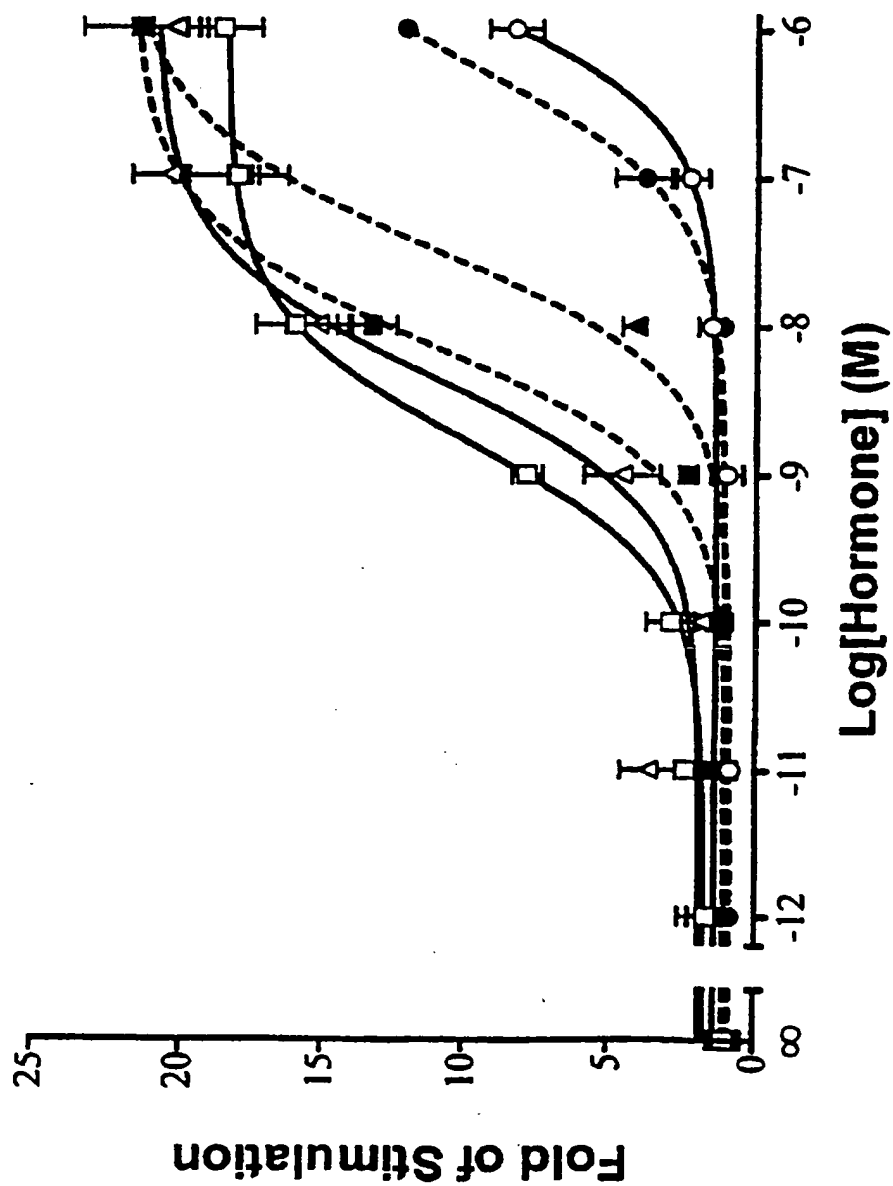
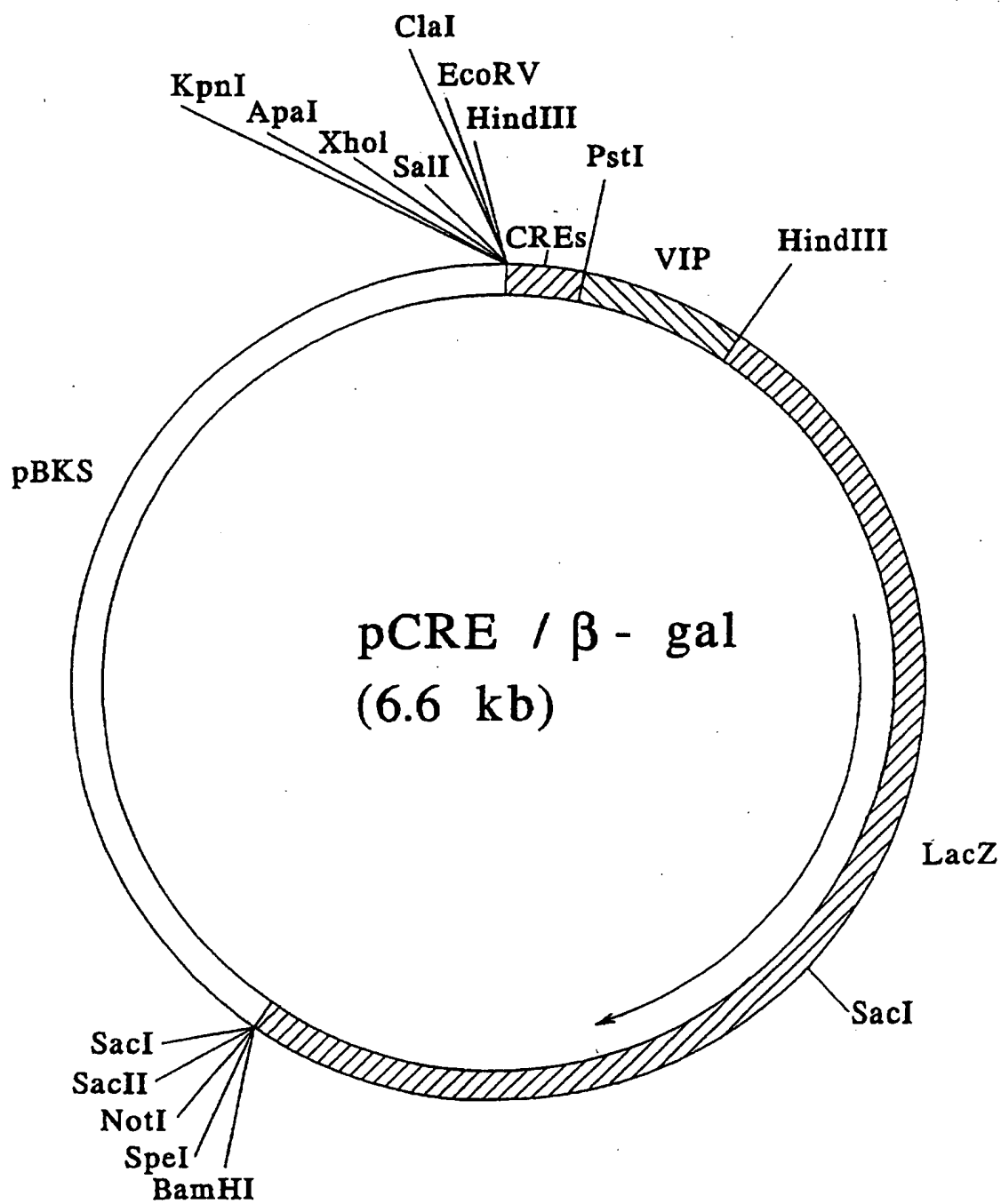
FIG. 13

FIG. 14

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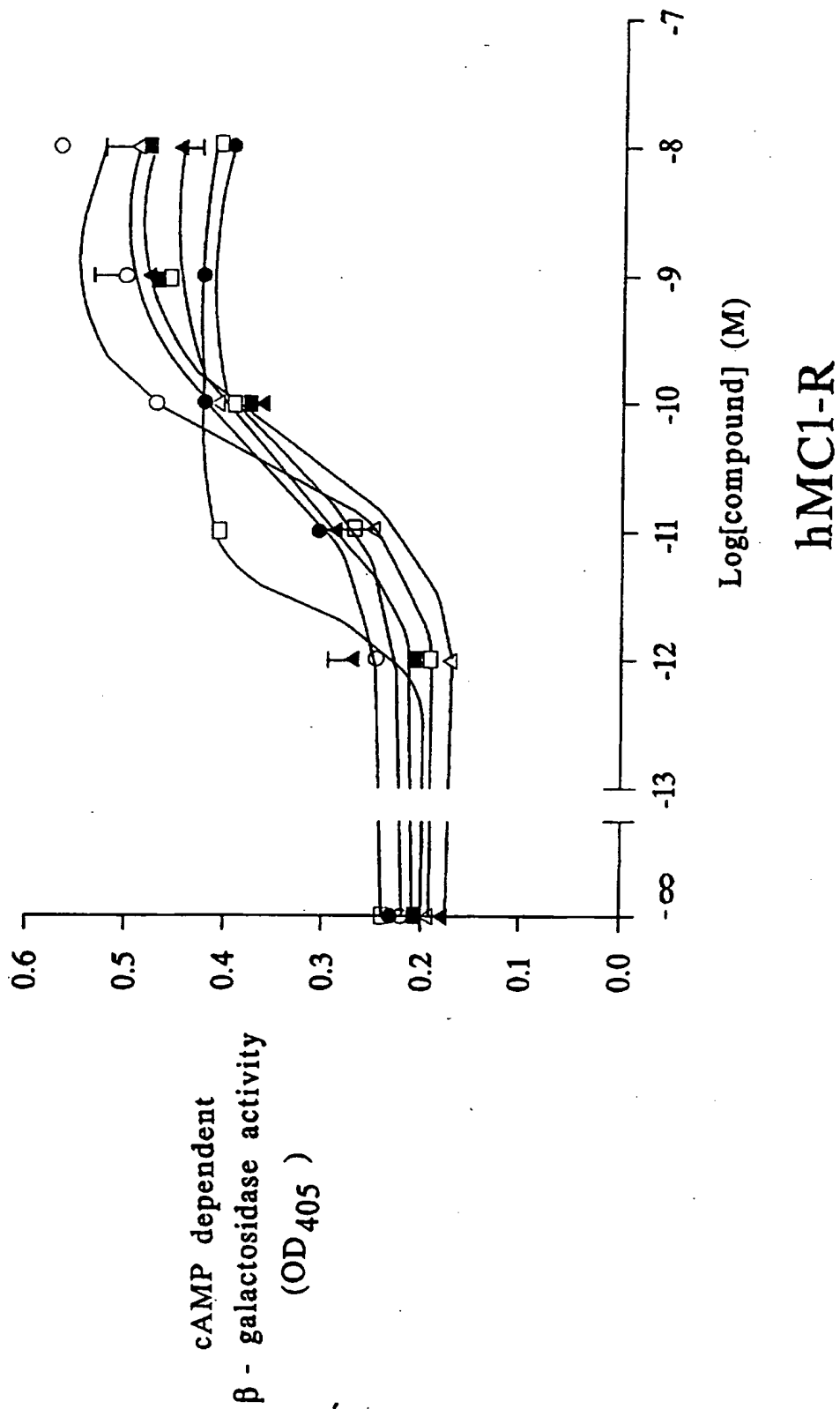
FIG. 15A

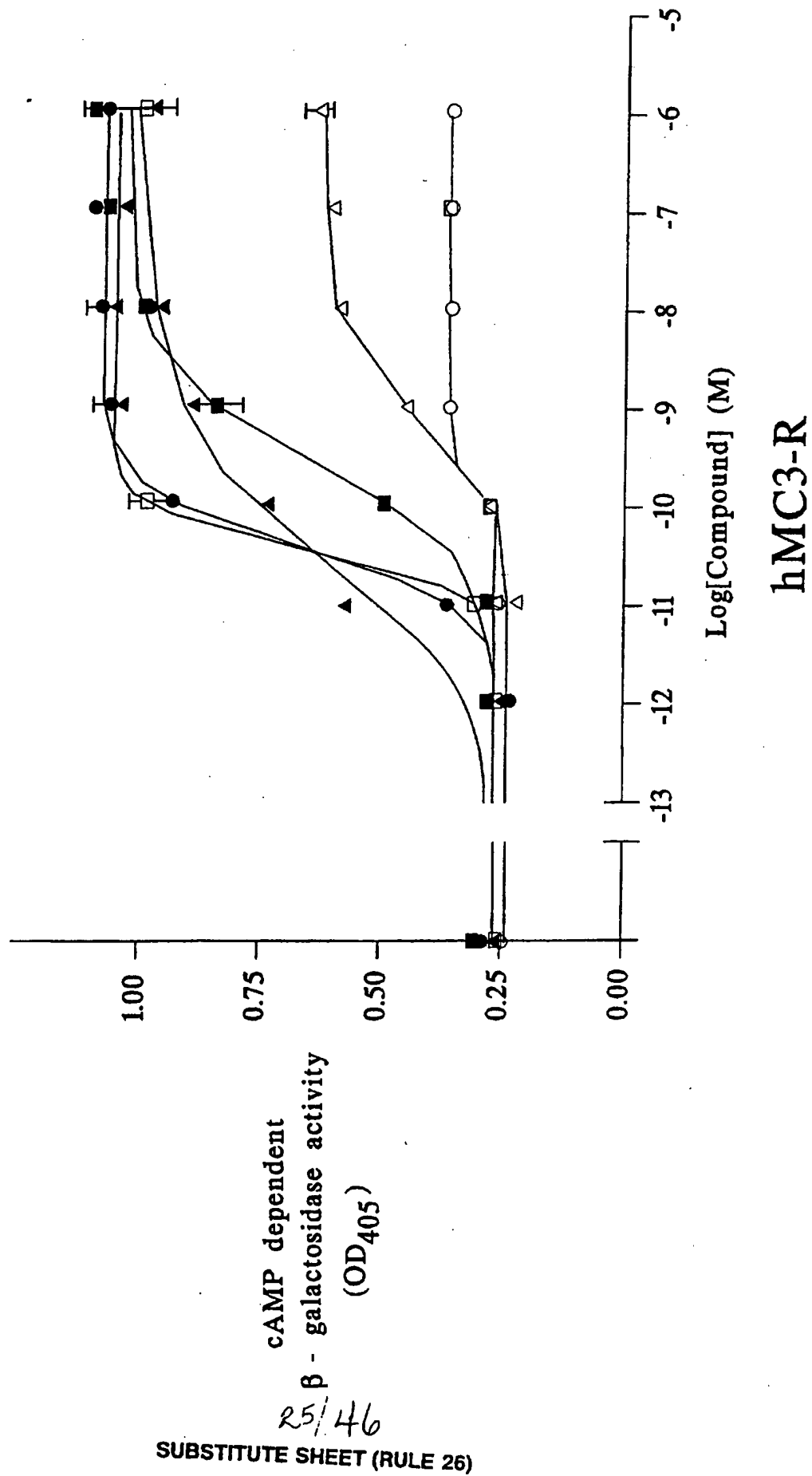
FIG. 15B

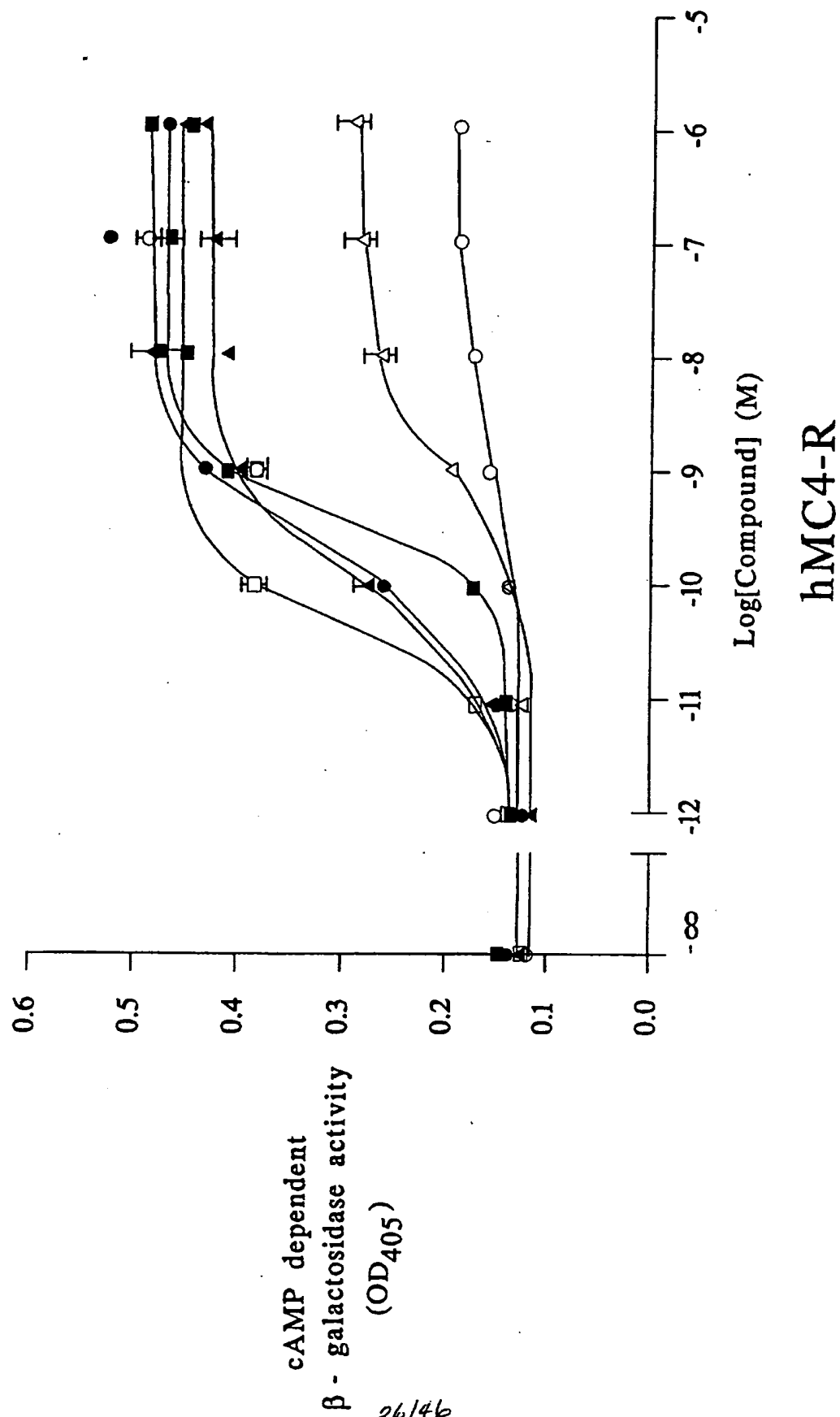
FIG. 15C

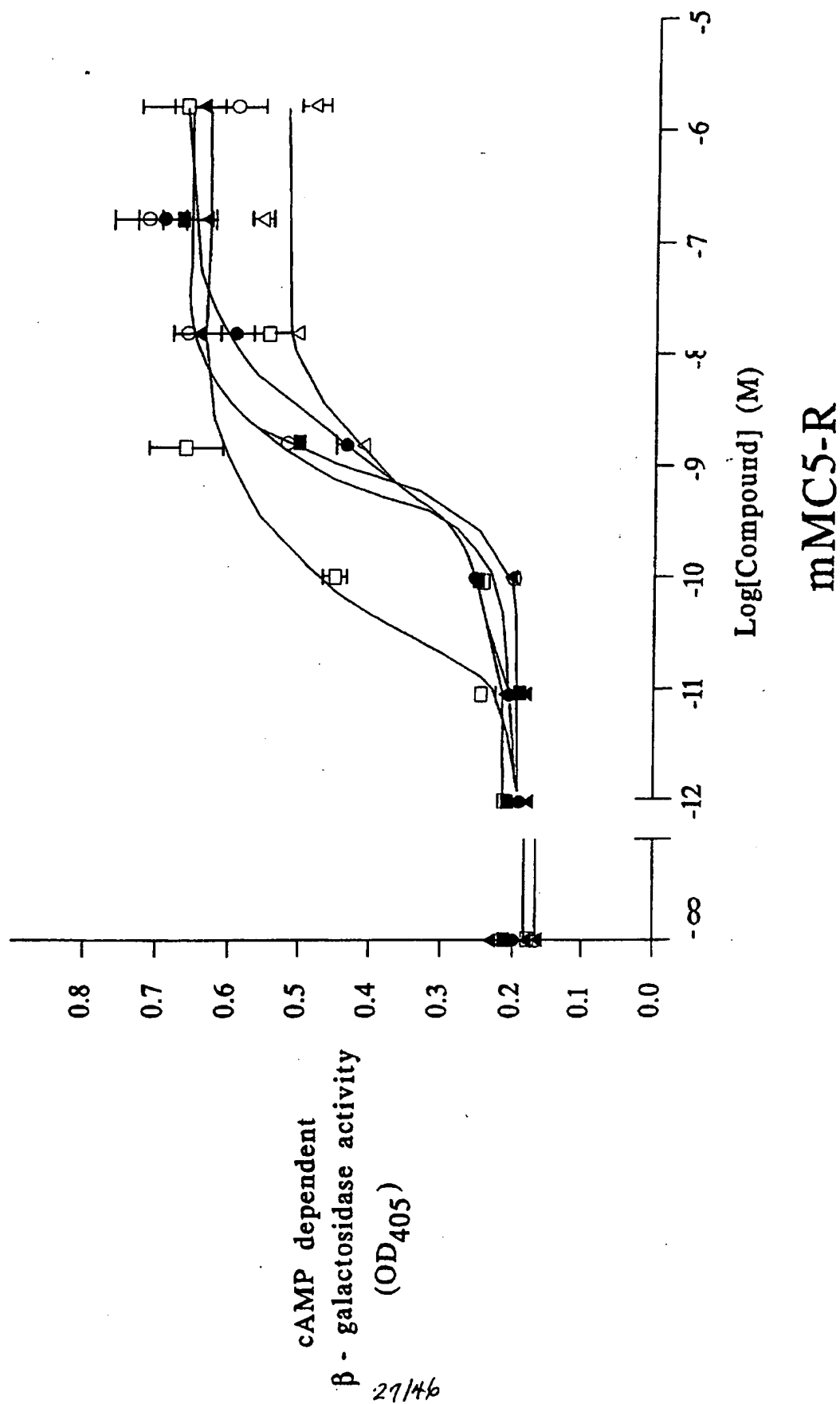
FIG. 15D

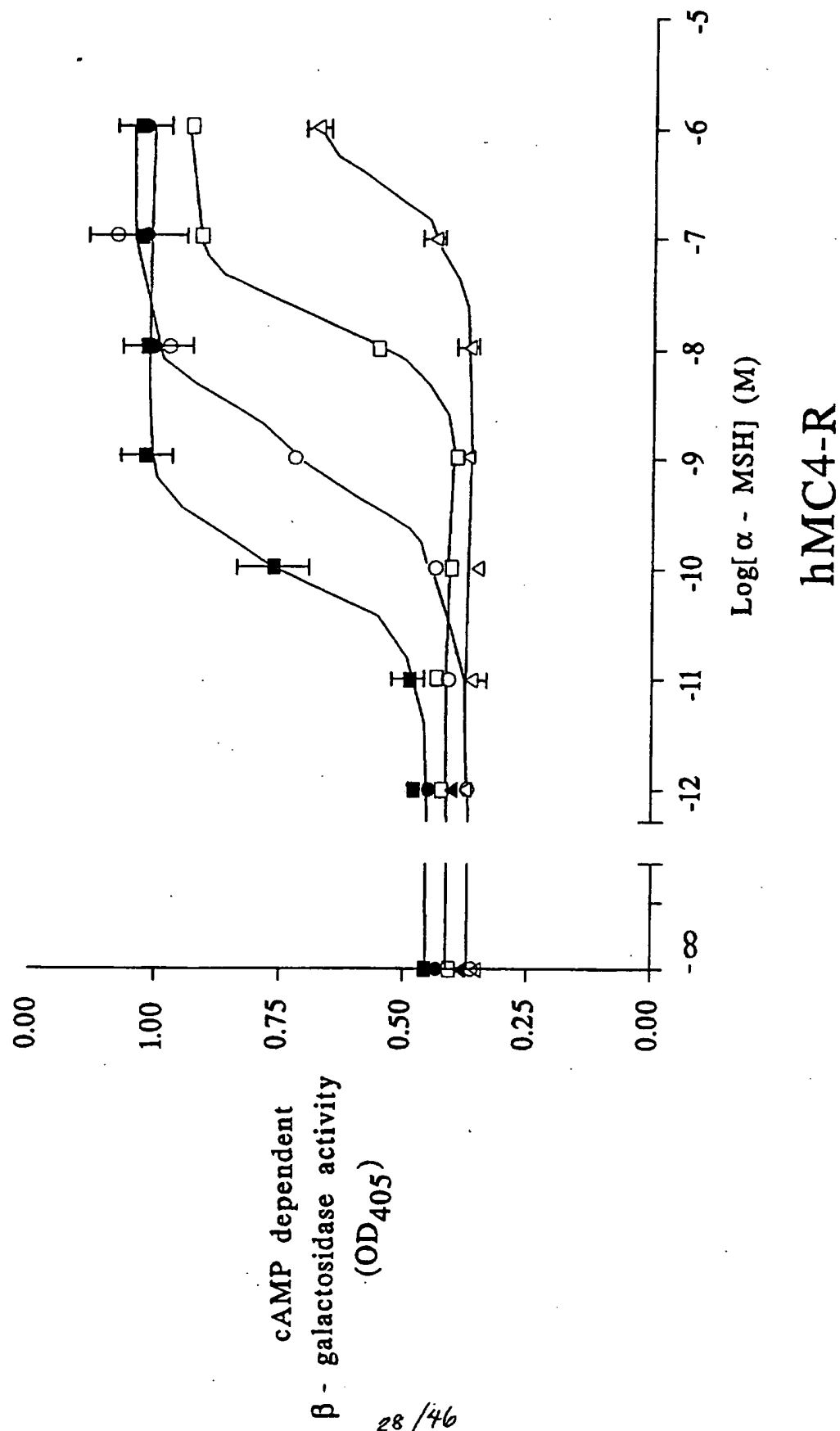
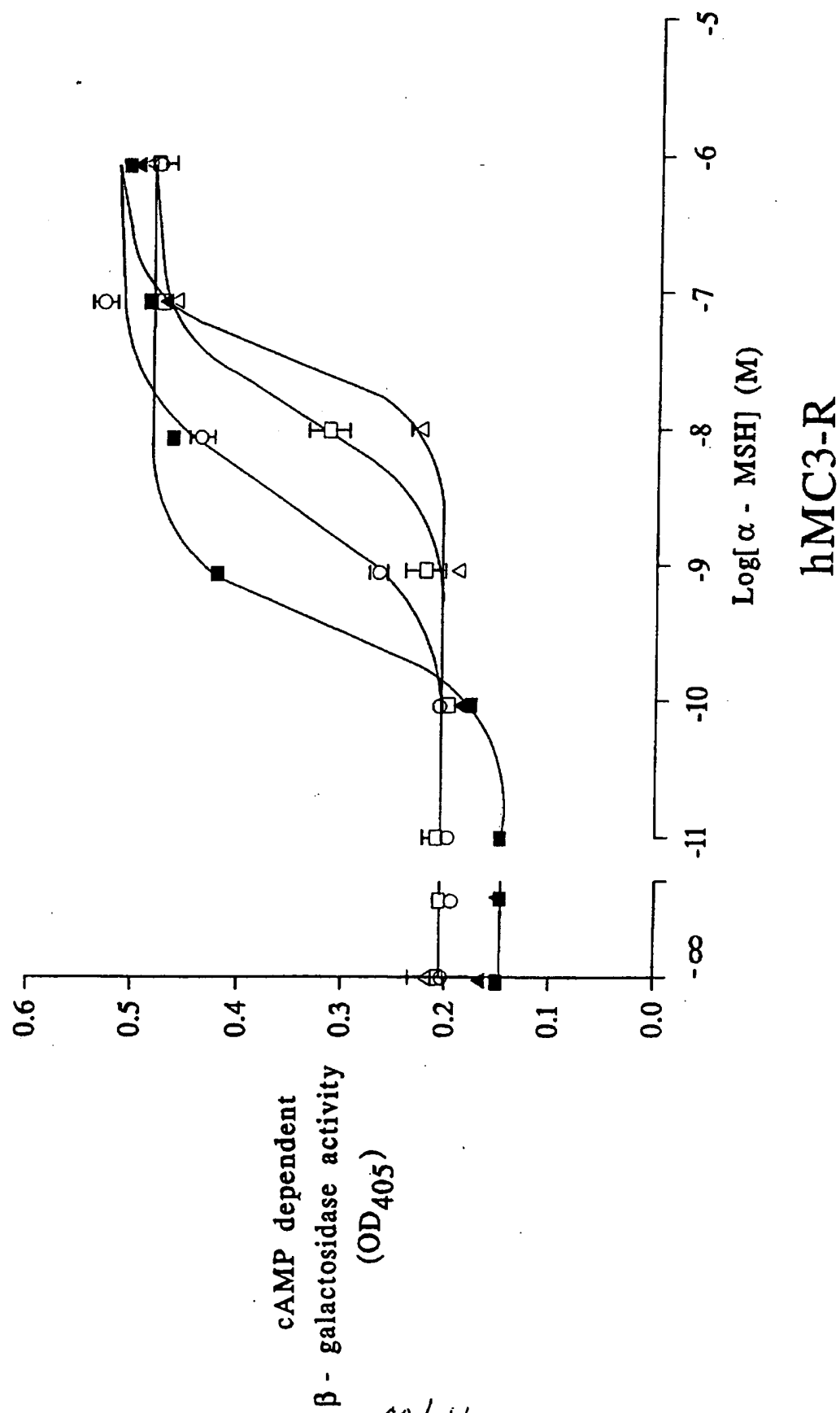
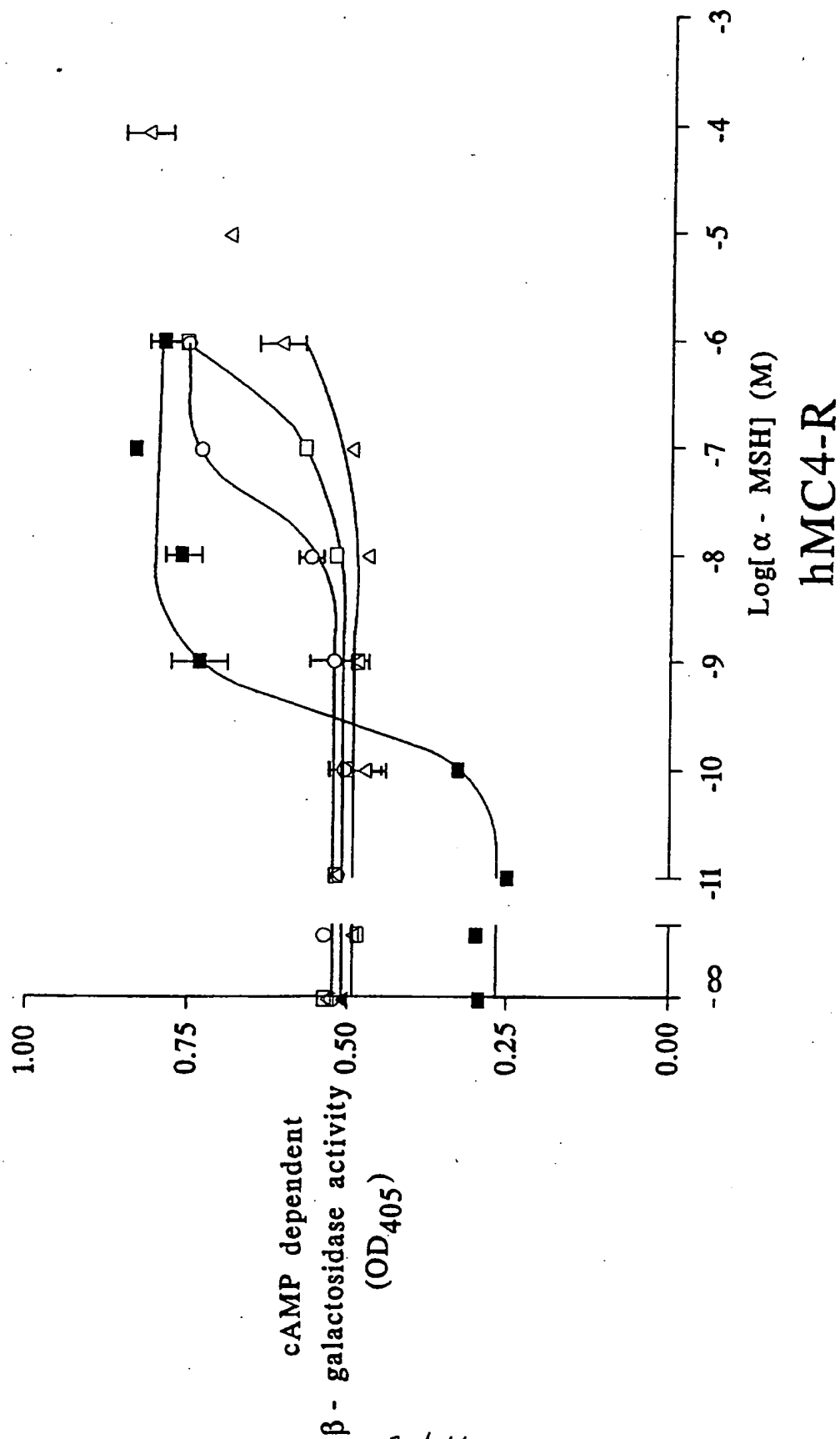
FIG. 16A

FIG. 16B

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FIG. 16C

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FIG. 16D

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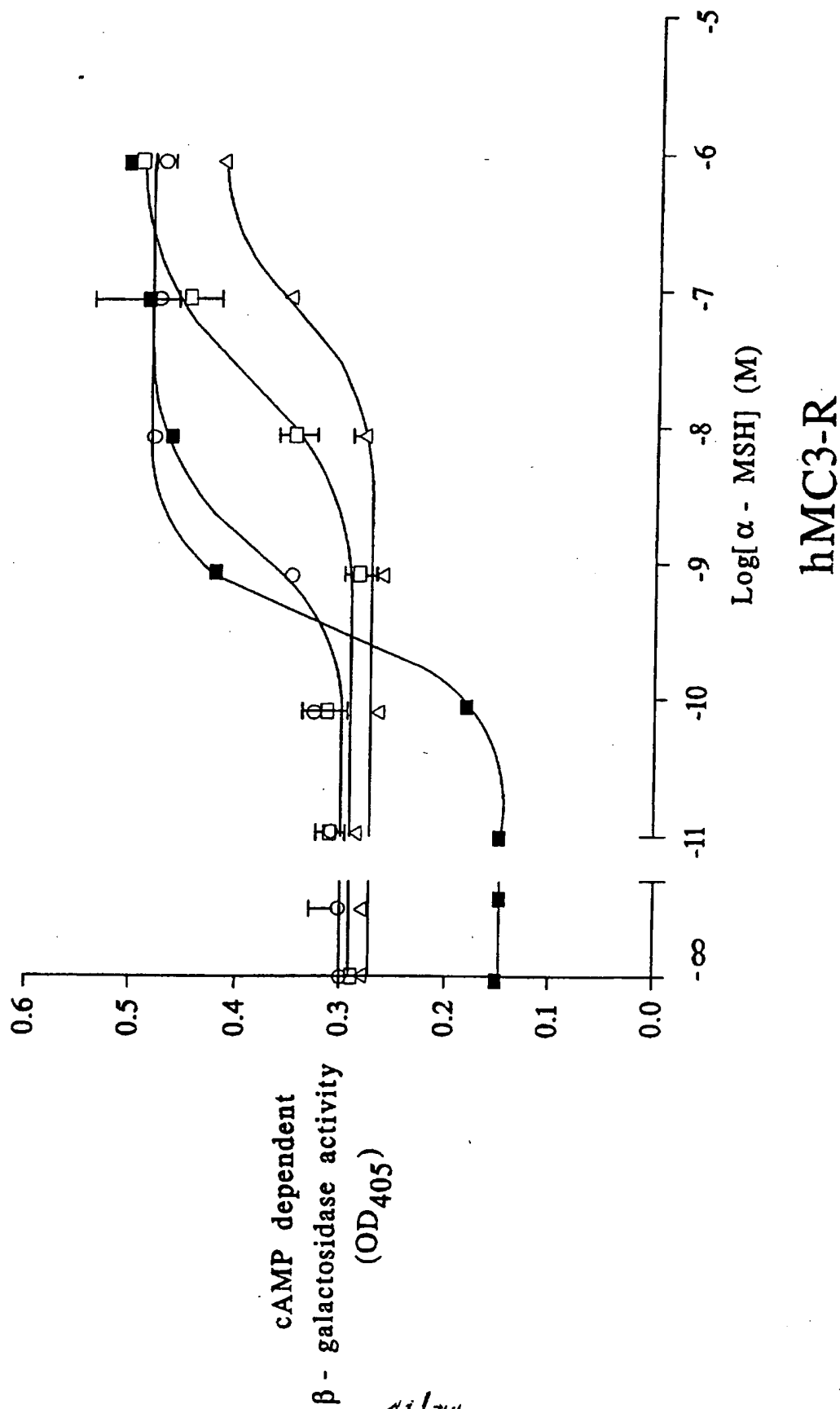
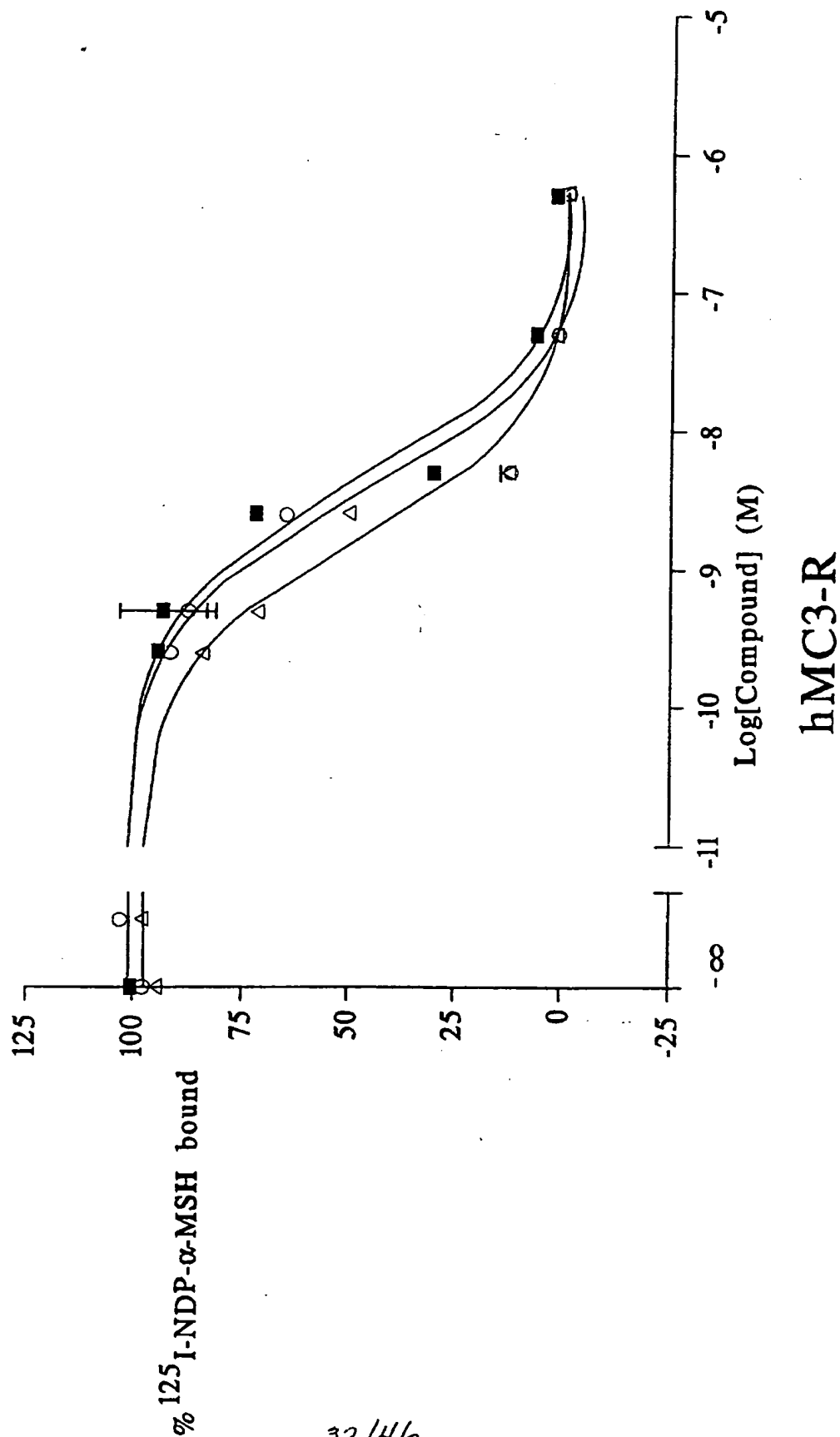
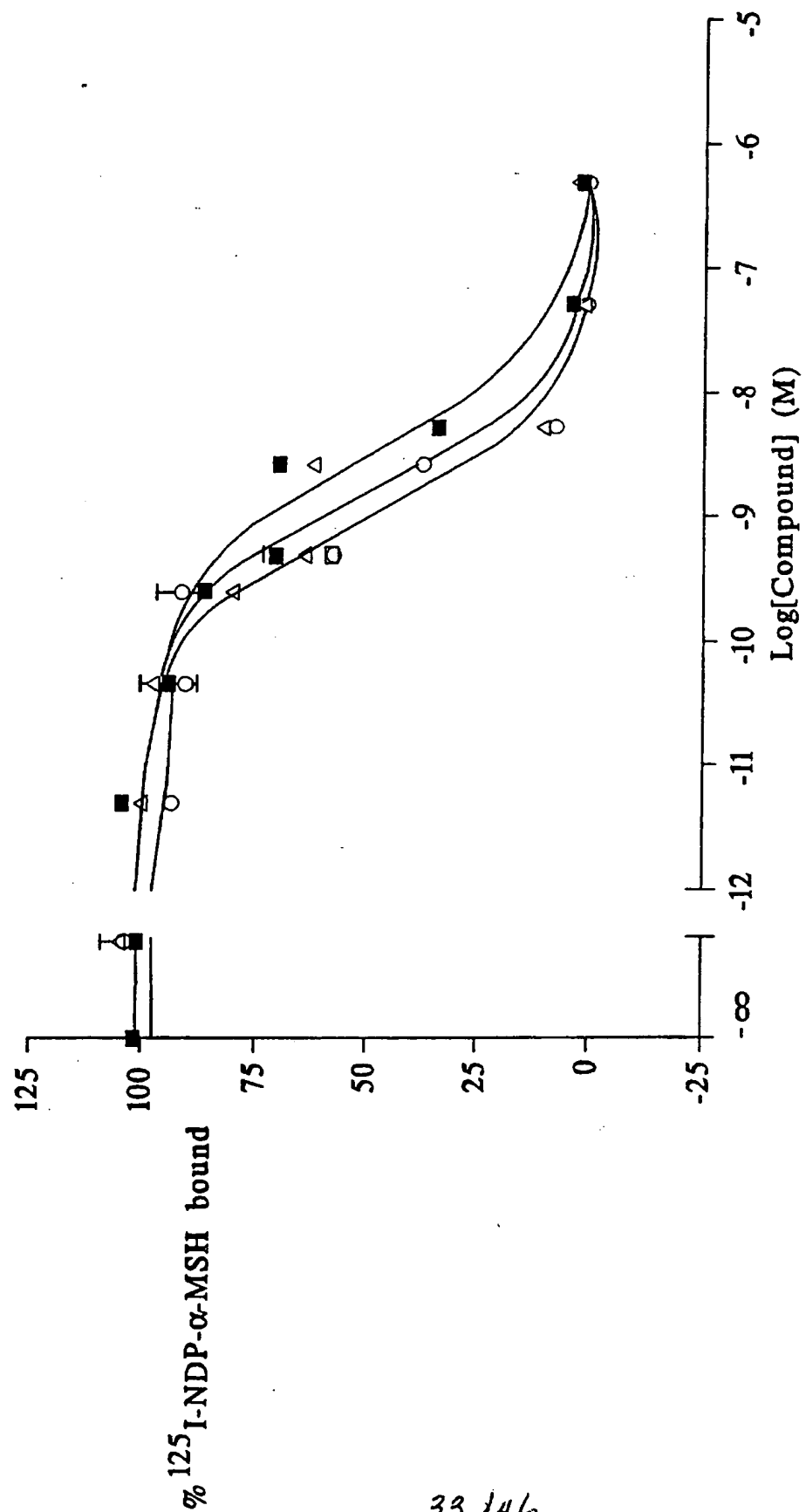
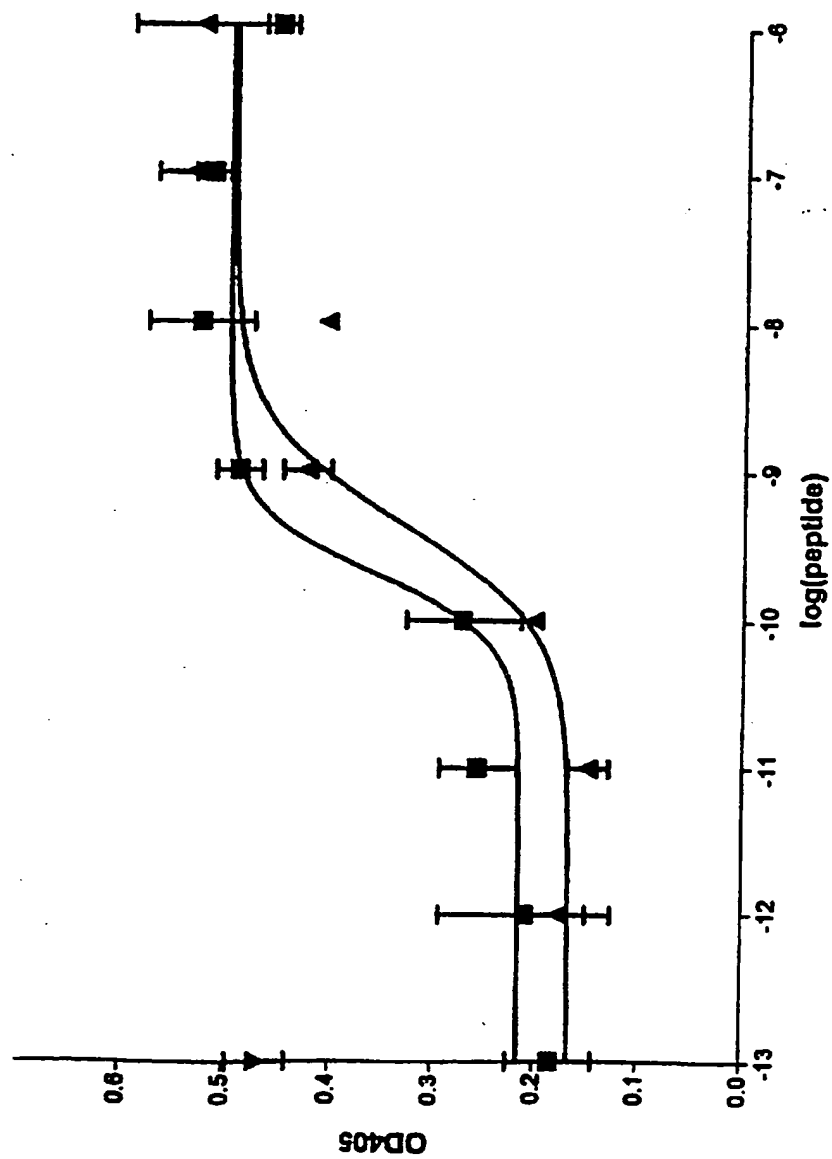


FIG. 17A

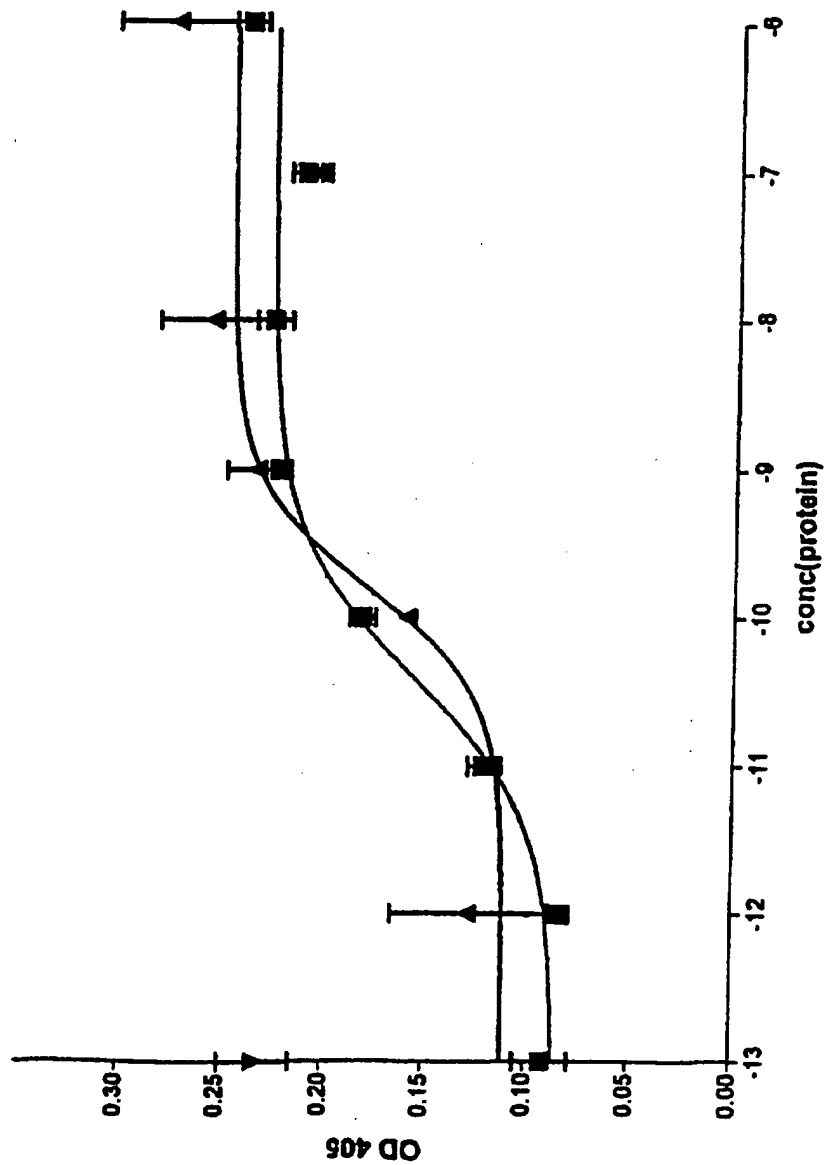
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FIG. 17B

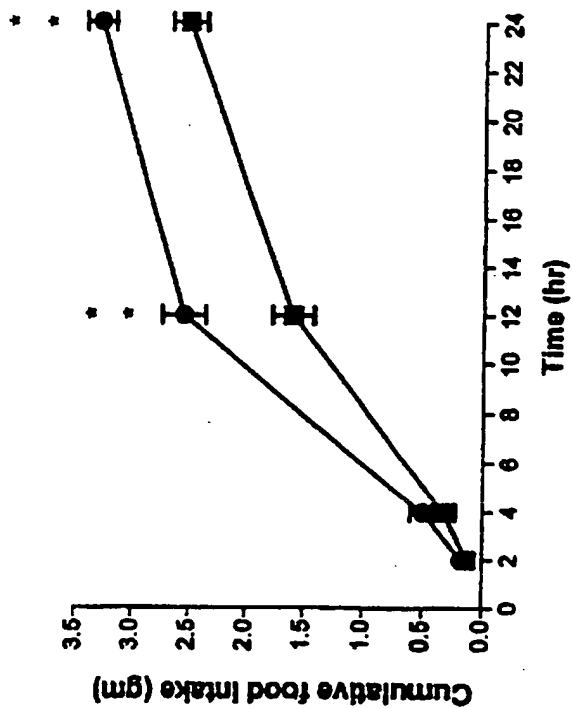
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FIG. 18A

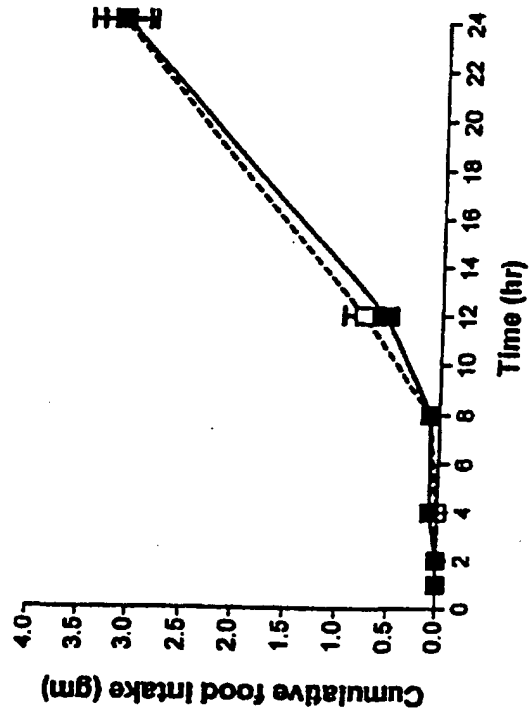
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FIG. 18B

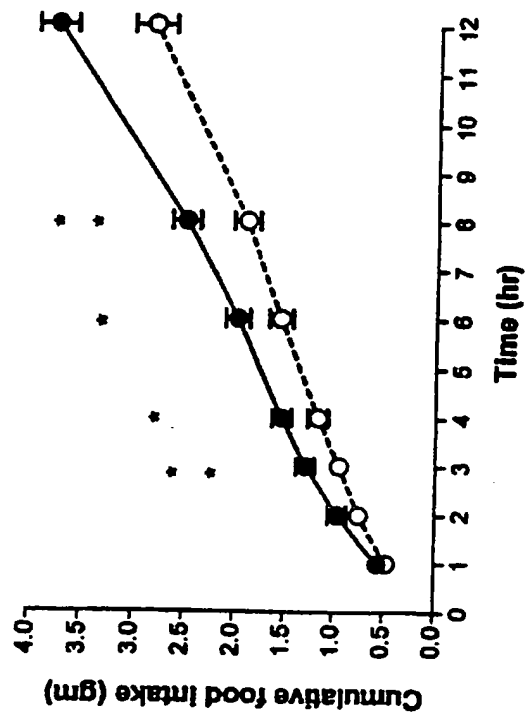
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FIG. 19A

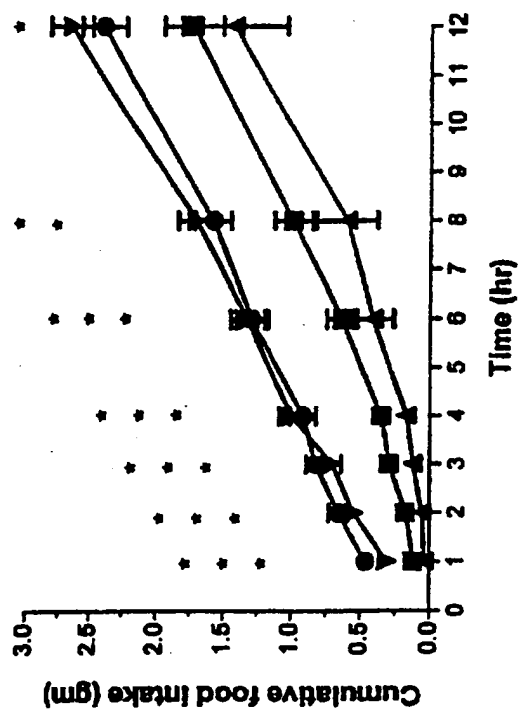
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FIG. 19B

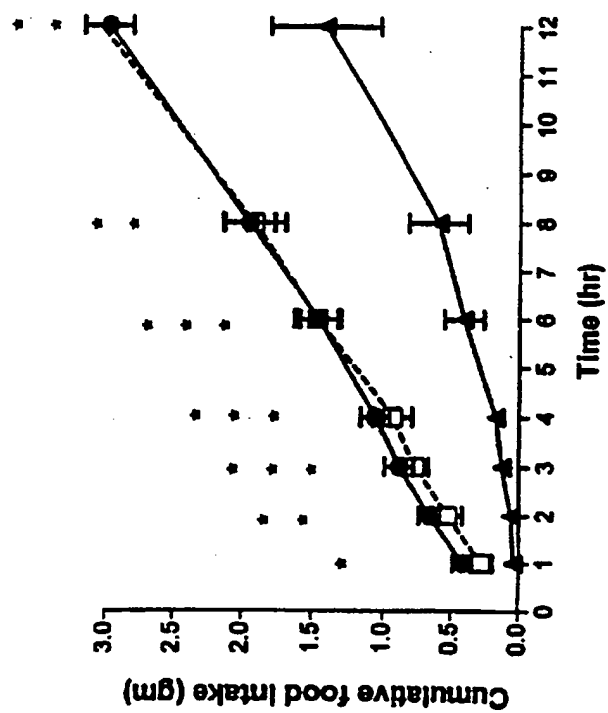
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FIG. 19C

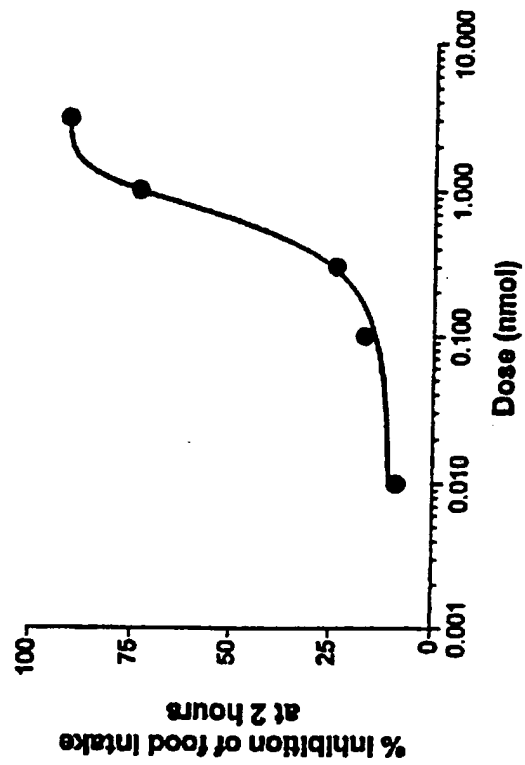
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FIG. 20A

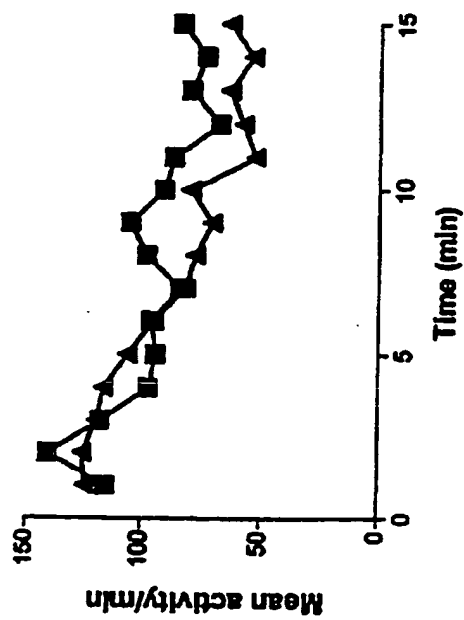
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FIG. 20B

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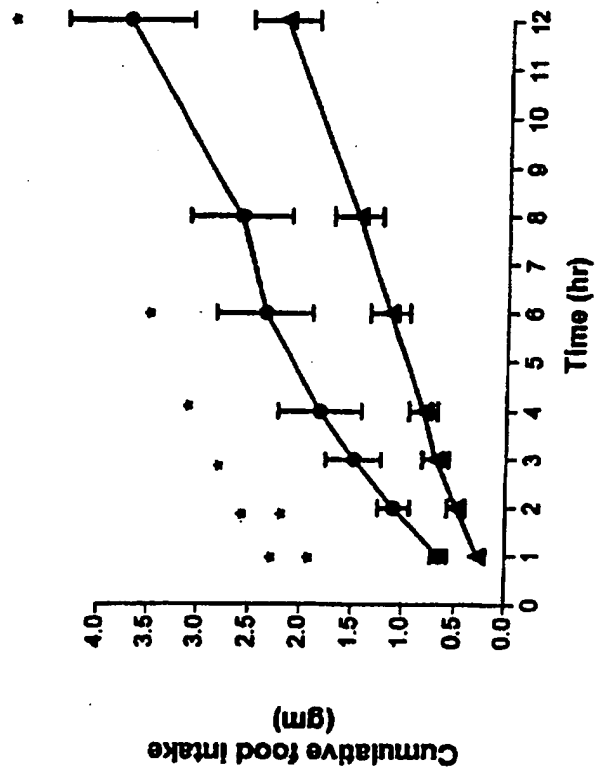
FIG. 20C

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FIG. 20D

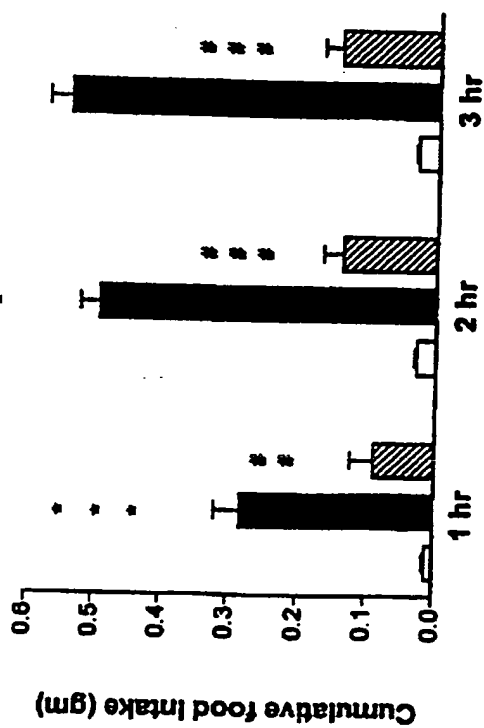
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FIG. 21A

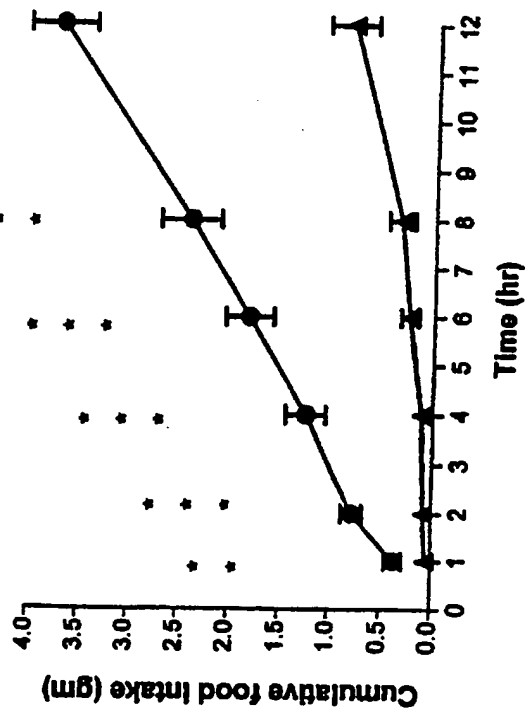


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FIG. 21B



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FIG. 21C

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FIG. 21D